

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 14, 2006, 21:02:04 ; Search time 46 Seconds  
(without alignments)  
938.189 Million cell updates/sec

Title: US-09-927-458-2  
Perfect score: 2754  
Sequence: 1 MRLVRLLKRTWPLEVPEPE.....DRPFPRSPRGRTDGRLSFM 522

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*

- 1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/PCRTUS\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2748	99.8	557	2	US-09-949-016-10867
2	2744	99.6	522	2	US-09-591-694-10
3	2489	90.4	482	2	US-09-385-219A-14
4	2270	82.4	443	2	US-09-591-694-8
5	553	20.1	102	2	US-09-621-976-5935
6	194	7.0	39	2	US-09-385-219A-21
7	189	6.9	38	2	US-09-172-841-47
8	189	6.9	38	2	US-09-951-621-47
9	164	6.0	38	2	US-09-172-841-49
10	164	6.0	38	2	US-09-951-621-49
11	144	5.2	321	2	US-09-166-350-15
12	139	5.0	327	2	US-09-591-694-12
13	139	5.0	327	2	US-09-385-219A-58
14	117.5	4.3	503	2	US-10-078-547-2
15	117.5	4.3	503	2	US-10-078-547-2
16	117	4.2	507	2	US-09-599-287A-24
17	117	4.2	507	2	US-10-078-547-24
18	112	4.1	690	2	US-09-248-796A-19169
19	111.5	4.0	506	2	US-09-949-016-11282
20	111.5	4.0	955	2	US-09-949-016-8369
21	111	4.0	406	2	US-10-104-047-3010
22	110.5	4.0	553	2	US-09-949-016-7961
23	110	4.0	424	2	US-09-538-092-1338
24	109	4.0	3730	2	US-09-949-016-9908
25	107.5	3.9	776	2	US-09-252-991A-28446
26	107	3.9	78	1	US-08-487-359-5
27	107	3.9	78	1	US-08-222-798A-5

28	107	3.9	489	2	US-09-543-681A-7388	Sequence 7388, Ap
29	107	3.9	557	2	US-09-949-016-7621	Sequence 7621, Ap
30	105	3.8	297	2	US-09-252-991A-29217	Sequence 29217, A
31	105	3.8	502	2	US-09-839-577A-14	Sequence 14, Appl
32	105	3.8	662	2	US-09-949-016-3186	Sequence 9186, Ap
33	105	3.8	1031	2	US-10-104-047-2327	Sequence 2327, Ap
34	104.5	3.8	850	2	US-09-949-016-11324	Sequence 11324, A
35	104	3.8	1312	2	US-09-554-572-26	Sequence 26, Appl
36	103.5	3.8	79	1	US-08-487-359-8	Sequence 8, Appl
37	103.5	3.8	79	1	US-08-222-798A-8	Sequence 8, Appl
38	103.5	3.8	580	2	US-08-966-865-1	Sequence 1, Appl
39	103.5	3.8	580	2	US-09-129-668-1	Sequence 1, Appl
40	103.5	3.8	888	1	US-08-861-464-6	Sequence 6, Appl
41	103.5	3.8	888	1	US-08-396-001-6	Sequence 6, Appl
42	103.5	3.8	888	2	US-09-323-433A-6	Sequence 6, Appl
43	103.5	3.8	888	2	US-08-826-752-6	Sequence 6, Appl
44	103	3.7	133	2	US-09-252-991A-21490	Sequence 21490, A
45	103	3.7	431	2	US-09-248-796A-17260	Sequence 17260, A

ALIGNMENTS

RESULT 1  
US-09-949-016-10867  
; Sequence 10867, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTIER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10867  
; LENGTH: 557  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-10867

Query Match	99.8%	Score	2748	DB 2	Length	557			
Best Local Similarity	99.8%	Pred. No.	2.2e-255						
Matches	521	Conservative	0	Mismatches	1	Indels	0	Gaps	0
Qy	1	MRLVRLLKRTWPLEVPEPETEPTLGHRLSHRLSLCTWGYSSNTRFTITLNYKDPPLTGDE	60						
Db	36	MRLVRLLKRTWPLEVPEPETEPTLGHRLSHRLSLCTWGYSSNTRFTITLNYKDPPLTGDE	95						
Qy	61	ETLASGIVSGDLICILQDDIPAPNIPSTDSHSSLQNNQPSLATSSNOTSMQDEQP	120						
Db	96	ETLASGIVSGDLICILQDDIPAPNIPSTDSHSSLQNNQPSLATSSNOTSMQDEQP	155						
Qy	121	SDSFQQAQSGVWDDSMGLPQNFQAEISIQDNAHMAEGTGFYPSEPMCLCSSEVGEQVP	180						
Db	156	SDSFQQAQSGVWDDSMGLPQNFQAEISIQDNAHMAEGTGFYPSEPMCLCSSEVGEQVP	215						
Qy	181	HSLETLYQSADCSANDALIVLIHLLMLSSGYIPQGTAKALSMPKRWKLSGVYKQYMH	240						
Db	216	HSLETLYQSADCSANDALIVLIHLLMLSSGYIPQGTAKALSMPKRWKLSGVYKQYMH	275						
Qy	241	PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFFICEKLGENVANYTKD	300						
Db	276	PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFFICEKLGENVANYTKD	335						
Qy	301	LQKLSRLFKDQIVVPLLAFTFQALNLPDVFGLVVLPLEIKLRIFRLLDVRSLVSLSAVCR	360						

Db 336 LQKLSRLFKDQVYVPLLAFTQAALNLPDVFGVLVPLELKLRIPELLDVRSVLSAVCR 395  
Qy 361 DLFTASNDPLLRWRELYLDRFDNDNTVRVQDQDWKELYRKHIORKESPKGRFVMLLPSSSTH 420  
Db 396 DLFTASNDPLLRWRELYLDRFDNDNTVRVQDQDWKELYRKHIORKESPKGRFVMLLPSSSTH 455  
Qy 421 TIPFVNPPLHPRPPSSRLPGCIIGGEYDQRTPLPVGDPISLLIPGGETPSQPPPLRP 480  
Db 456 TIPFVNPPLHPRPPSSRLPGCIIGGEYDQRTPLPVGDPISLLIPGGETPSQPPPLRP 515  
Qy 481 RFDVPGLPGNPILPGRGGNDPFRPPSPRGRPTDGRLSFM 522  
Db 516 RFDVPGLPGNPILPGRGGNDPFRPPSPRGRPTDGRLSFM 557

RESULT 2  
US-09-591-694-10  
; Sequence 10, Application US/09591694  
; Patent No. 6638734  
; GENERAL INFORMATION:  
; APPLICANT: John C. Reed  
; APPLICANT: Shu-ichi Matsuzawa  
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved  
; TITLE OF INVENTION: in Protein Degradation, Products and Methods Related Thereto  
; FILE REFERENCE: P-LJ 4220  
; CURRENT APPLICATION NUMBER: US/09/591,694  
; CURRENT FILING DATE: 2000-06-09  
; EARLIER APPLICATION NUMBER: US 09/330,517  
; EARLIER FILING DATE: 1999-06-11  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 522  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-09-591-694-10

Query Match 99.6%; Score 2744; DB 2; Length 522;  
Best Local Similarity 99.6%; Pred. No. 4.8e-255;  
Matches 520; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRLRVLLKRTWPLEVPETPTLGHRLSHLRLSLCTWGYSSNTFTITLNYKDLPTGDE 60  
Db 1 MRLRVLLKRTWPLEVPETPTLGHRLSHLRLSLCTWGYSSNTFTITLNYKDLPTGDE 60  
Qy 61 ETLASYGIVSGDLICLILODDIPAPNIPSSSTDSEHSLQNNNEQPSLATSSNQTSMQDEQP 120  
Db 61 ETLASYGIVSGDLICLILODDIPAPNIPSSSTDSEHSLQNNNEQPSLATSSNQTSMQDEQP 120  
Qy 121 SDSFGQAAQSGVWDDSMLGPSQNFEAESIQDNAHMAEGTGFYSEPMLCSESVEGQVP 180  
Db 121 SDSFGQAAQSGVWDDSMLGPSQNFEAESIQDNAHMAEGTGFYSEPMLCSESVEGQVP 180  
Qy 181 HSLETLYQSADCSANDALIIVLIHLLMESGYIPOGTEAKALSMPEKWKLSGVYKLQYMH 240  
Db 181 HSLETLYQSADCSANDALIIVLIHLLMESGYIPOGTEAKALSMPEKWKLSGVYKLQYMH 240  
Qy 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFTICEKLGENVANIYKD 300  
Db 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFTICEKLGENVANIYKD 300  
Qy 301 LOKLSRLFKDQVYVPLLAFTQAALNLPDVFGVLVPLELKLRIPELLDVRSVLSAVCR 360  
Db 301 LOKLSRLFKDQVYVPLLAFTQAALNLPDVFGVLVPLELKLRIPELLDVRSVLSAVCR 360  
Qy 361 DLFTASNDPLLRWRELYLDRFDNDNTVRVQDQDWKELYRKHIORKESPKGRFVMLLPSSSTH 420  
Db 361 DLFTASNDPLLRWRELYLDRFDNDNTVRVQDQDWKELYRKHIORKESPKGRFVMLLPSSSTH 420  
Qy 421 TIPFVNPPLHPRPPSSRLPGCIIGGEYDQRTPLPVGDPISLLIPGGETPSQPPPLRP 480  
Db 421 TIPFVNPPLHPRPPSSRLPGCIIGGEYDQRTPLPVGDPISLLIPGGETPSQPPPLRP 480

Qy 481 RFDVPGLPGNPILPGRGGNDPFRPPSPRGRPTDGRLSFM 522  
Db 481 RFDVPGLPGNPILPGRGGNDPFRPPSPRGRPTDGRLSFM 522

RESULT 3  
US-09-385-219A-14  
; Sequence 14, Application US/09385219A  
; Patent No. 6720181  
; GENERAL INFORMATION:  
; APPLICANT: Chiaux, D.  
; APPLICANT: Pagano, M.  
; APPLICANT: Latres, E.  
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS  
; FILE REFERENCE: 5914-081  
; CURRENT APPLICATION NUMBER: US/09/385,219A  
; CURRENT FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: 60/098,355  
; PRIOR FILING DATE: 1998-08-28  
; PRIOR APPLICATION NUMBER: 60/118,568  
; PRIOR FILING DATE: 1999-02-03  
; PRIOR APPLICATION NUMBER: 60/124,449  
; PRIOR FILING DATE: 1999-03-15  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 482  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-385-219A-14

Query Match 90.4%; Score 2489; DB 2; Length 482;  
Best Local Similarity 98.1%; Pred. No. 1.5e-230;  
Matches 472; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 42 SNTRFTITLNYKDLPTGDEETLASYGIVSGDLICLILODDIPAPNIPSSSTDSEHSSLQNN 101  
Db 2 SNTRFTITLNYKDLPTGDEETLASYGIVSGDLICLILODDIPAPNIPSSSTDSEHSSLQNN 61  
Qy 102 EQPSLATSSNQTSMQDEQPSDSFGQAAQSGVWDDSMLGPSQNFEAESIQDNAHMAEGT 161  
Db 62 EQPSLATSSNQTSMQDEQPSDSFGQAAQSGVWDDSMLGPSQNFEAESIQDNAHMAEGT 121  
Qy 162 GFYSEPMLCSESVEGQVPHSLETLYQSADCSANDALIIVLIHLLMESGYIPOGTEAKA 221  
Db 122 GFYSEPMLCSESVEGQVPHSLETLYQSADCSANDALIIVLIHLLMESGYIPOGTEAKA 181  
Qy 222 LSMPEKWKLSGVYKLQYMHPLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLP 281  
Db 182 LSMPEKWKLSGVYKLQYMHPLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLP 241  
Qy 282 ESFTICEKLGENVANIYKDLOKLSRLFKDQVYVPLLAFTQAALNLPDVFGVLVPLELKL 341  
Db 242 ESFTICEKLGENVANIYKDLOKLSRLFKDQVYVPLLAFTQAALNLPDVFGVLVPLELKL 301  
Qy 342 RIFRLLDVRSVLSAVCRDLFTASNDPLLRWRELYLDRFDNDNTVRVQDQDWKELYRKRHI 401  
Db 302 RIFRLLDVRSVLSAVCRDLFTASNDPLLRWRELYLDRFDNDNTVRVQDQDWKELYRKRHI 361  
Qy 402 QRKESPKGRFVMLLPSSSTHTTIPFVNPPLHPRPPSSRLPGCIIGGEYDQRTPLPVGDPI 461  
Db 362 QRKESPKGRFVMLLPSSSTHTTIPFVNPPLHPRPPSSRLPGCIIGGEYDQRTPLPVGDPI 421  
Qy 462 SSLIPGGETPSQPPPLRPFRDPVGPDPGPNPILPGRGGNDPFRPPSPRGRPTDGRLSF 521  
Db 422 SSLIPGGETPSQPPPLRPFRDPVGPDPGPNPILPGRGGNDPFRPPSPRGRPTDGRLSF 481  
Qy 522 M 522  
Db 482 M 482

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RESULT 4
US-09-591-694-8
; Sequence 8, Application US/09591694
; Patent No. 6638734
; GENERAL INFORMATION:
; APPLICANT: John C. Reed
; APPLICANT: Shu-ichi Matsuzawa
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved
; FILE OF INVENTION: In Protein Degradation, Products and Methods Related Thereto
; FILE REFERENCE: P-LJ 4220
; CURRENT APPLICATION NUMBER: US/09/591.694
; CURRENT FILING DATE: 2000-06-09
; EARLIER APPLICATION NUMBER: US 09/330.517
; EARLIER FILING DATE: 1999-06-11
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-591-694-8

Query Match      82.4%; Score 2270; DB 2; Length 443;
Best Local Similarity 99.8%; Pred. No. 1.5e-209;
Matches 430; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 92 DSEHSSLQNNQPSLATSSNQTSMQDEQPSDSFGQAAQSGVWDDSMLGPSQNFAEESI 151
Db 13 DSEHSSLQNNQPSLATSSNQTSMQDEQPSDSFGQAAQSGVWDDSMLGPSQNFAEESI 72

Qy 152 QDNAMAEAGTGFPSEPMLCSESVGQVPHSLFTLYQSADCSNDALIVLHLLMLES 211
Db 73 QDNAMAEAGTGFPSEPMLCSESVGQVPHSLFTLYQSADCSNDALIVLHLLMLES 132

Qy 212 YIPGTTAKALSMPEKKWLSGVYKLYMHPLCEGSSATLCVPLGNLIVVNATUKINNEI 271
Db 133 YIPGTTAKALSMPEKKWLSGVYKLYMHPLCEGSSATLCVPLGNLIVVNATUKINNEI 192

Qy 272 RSVKRLQLLPESFICKEKLGENVANIYKDLQKLSRLFKDLVYPLLAFTQALNLPDVF 331
Db 193 RSVKRLQLLPESFICKEKLGENVANIYKDLQKLSRLFKDLVYPLLAFTQALNLPDVF 252

Qy 332 LVVLPLELKLRIFFLLDVRSLSVAVCRDLFTASNDPLLRFLYLRDRDNTVRVQD 391
Db 253 LVVLPLELKLRIFFLLDVRSLSVAVCRDLFTASNDPLLRFLYLRDRDNTVRVQD 312

Qy 392 WKELYRKRHIQRKESPKGRFVMLLPSSHTTTPFYPNPLHRRPPSSRLPGCIIGGYD 451
Db 313 WKELYRKRHIQRKESPKGRFVMLLPSSHTTTPFYPNPLHRRPPSSRLPGCIIGGYD 372

Qy 452 PTLPYVGDPISLLIPGGETPSQFPPLRPDPVGPPLPGNPILPGRGGPNDRPFPSPSR 511
Db 373 PTLPYVGDPISLLIPGGETPSQFPPLRPDPVGPPLPGNPILPGRGGPNDRPFPSPSR 432

Qy 512 GRPTDGRLSFM 522
Db 433 GRPTDGRLSFM 443

RESULT 5
US-09-621-976-5935
; Sequence 5935, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm

Query Match      82.4%; Score 2270; DB 2; Length 443;
Best Local Similarity 99.8%; Pred. No. 1.5e-209;
Matches 430; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 92 DSEHSSLQNNQPSLATSSNQTSMQDEQPSDSFGQAAQSGVWDDSMLGPSQNFAEESI 151
Db 13 DSEHSSLQNNQPSLATSSNQTSMQDEQPSDSFGQAAQSGVWDDSMLGPSQNFAEESI 72

Qy 152 QDNAMAEAGTGFPSEPMLCSESVGQVPHSLFTLYQSADCSNDALIVLHLLMLES 211
Db 73 QDNAMAEAGTGFPSEPMLCSESVGQVPHSLFTLYQSADCSNDALIVLHLLMLES 132

Qy 212 YIPGTTAKALSMPEKKWLSGVYKLYMHPLCEGSSATLCVPLGNLIVVNATUKINNEI 271
Db 133 YIPGTTAKALSMPEKKWLSGVYKLYMHPLCEGSSATLCVPLGNLIVVNATUKINNEI 192

Qy 272 RSVKRLQLLPESFICKEKLGENVANIYKDLQKLSRLFKDLVYPLLAFTQALNLPDVF 331
Db 193 RSVKRLQLLPESFICKEKLGENVANIYKDLQKLSRLFKDLVYPLLAFTQALNLPDVF 252

Qy 332 LVVLPLELKLRIFFLLDVRSLSVAVCRDLFTASNDPLLRFLYLRDRDNTVRVQD 391
Db 253 LVVLPLELKLRIFFLLDVRSLSVAVCRDLFTASNDPLLRFLYLRDRDNTVRVQD 312

Qy 392 WKELYRKRHIQRKESPKGRFVMLLPSSHTTTPFYPNPLHRRPPSSRLPGCIIGGYD 451
Db 313 WKELYRKRHIQRKESPKGRFVMLLPSSHTTTPFYPNPLHRRPPSSRLPGCIIGGYD 372

Qy 452 PTLPYVGDPISLLIPGGETPSQFPPLRPDPVGPPLPGNPILPGRGGPNDRPFPSPSR 511
Db 373 PTLPYVGDPISLLIPGGETPSQFPPLRPDPVGPPLPGNPILPGRGGPNDRPFPSPSR 432

Qy 512 GRPTDGRLSFM 522
Db 433 GRPTDGRLSFM 443

RESULT 6
US-09-385-219A-21
; Sequence 21, Application US/09385219A
; Patent No. 6720181
; GENERAL INFORMATION:
; APPLICANT: Chiaux, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/09/385.219A
; CURRENT FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-385-219A-21

Query Match      7.0%; Score 194; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.8e-11;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 335 LPLELKLRIFFLLDVRSLSVAVCRDLFTASNDPLLR 373
Db 1 LPLELKLRIFFLLDVRSLSVAVCRDLFTASNDPLLR 39

RESULT 7
US-09-172-841-47
; Sequence 47, Application US/09172841
; Patent No. 6232081
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeffrey W.
; APPLICANT: Elledge, Stephen J.
; TITLE OF INVENTION: F-BOX PROTEINS AND GENES
; FILE REFERENCE: BCM-03510
; CURRENT APPLICATION NUMBER: US/09/172.841
; CURRENT FILING DATE: 1998-10-15
; EARLIER APPLICATION NUMBER: 08/951,621
; EARLIER FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 5935.
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 87
; OTHER INFORMATION: Xaa = Cys,Gly
US-09-621-976-5935

Query Match      20.1%; Score 553; DB 2; Length 102;
Best Local Similarity 99.0%; Pred. No. 2.4e-45;
Matches 98; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 413 MLLPSSTHTTIPFYFNPLHRRPPSSRLPGIIGGYDQRTPLPVGDPISLLIPGGETP 472
Db 1 MLLPSSTHTTIPFYFNPLHRRPPSSRLPGIIGGYDQRTPLPVGDPISLLIPGGETP 60

Qy 473 SQFPPLRPDPVGPPLPGNPILPGRGGPNDRPFPSPSR 511
Db 61 SQFPPLRPDPVGPPLPGNPILPGRGGPNDRPFPSPSR 99

RESULT 6
US-09-385-219A-21
; Sequence 21, Application US/09385219A
; Patent No. 6720181
; GENERAL INFORMATION:
; APPLICANT: Chiaux, D.
; APPLICANT: Pagano, M.
; APPLICANT: Latres, E.
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
; FILE REFERENCE: 5914-081
; CURRENT APPLICATION NUMBER: US/09/385.219A
; CURRENT FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1999-03-15
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-385-219A-21

Query Match      7.0%; Score 194; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.8e-11;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 335 LPLELKLRIFFLLDVRSLSVAVCRDLFTASNDPLLR 373
Db 1 LPLELKLRIFFLLDVRSLSVAVCRDLFTASNDPLLR 39

RESULT 7
US-09-172-841-47
; Sequence 47, Application US/09172841
; Patent No. 6232081
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeffrey W.
; APPLICANT: Elledge, Stephen J.
; TITLE OF INVENTION: F-BOX PROTEINS AND GENES
; FILE REFERENCE: BCM-03510
; CURRENT APPLICATION NUMBER: US/09/172.841
; CURRENT FILING DATE: 1998-10-15
; EARLIER APPLICATION NUMBER: 08/951,621
; EARLIER FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 47
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-172-841-47

Query Match          6.9%; Score 189; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 5.2e-11;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 335 LPLEKLRIFRLDVRVSLSAVCRDLFTASNDPLW 372
      |||||
Db 1 LPLEKLRIFRLDVRVSLSAVCRDLFTASNDPLW 38

RESULT 8
US-08-951-621-47
; Sequence 47, Application US/08951621
; Patent No. 6573094
; GENERAL INFORMATION:
; APPLICANT: HARPER, JEFFREY W.
; APPLICANT: ELLEDGE, STEPHEN J.
; TITLE OF INVENTION: F-BOX GENES AND PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/951,621
; FILING DATE: 16-OCT-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: BCM-02999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
US-08-951-621-47

Query Match          6.9%; Score 189; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 5.2e-11;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 335 LPLEKLRIFRLDVRVSLSAVCRDLFTASNDPLW 372
      |||||
Db 1 LPLEKLRIFRLDVRVSLSAVCRDLFTASNDPLW 38

RESULT 9
US-09-172-841-49
; Sequence 49, Application US/09172841
; Patent No. 6232081
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeffrey W.
; APPLICANT: Elledge, Stephen J.
; TITLE OF INVENTION: F-BOX PROTEINS AND GENES
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; FILE REFERENCE: BCM-03510
; CURRENT APPLICATION NUMBER: US/09/172,841
; CURRENT FILING DATE: 1998-10-15
; EARLIER APPLICATION NUMBER: 08/951,621
; EARLIER FILING DATE: 1997-10-16
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-172-841-49

Query Match          6.0%; Score 164; DB 2; Length 38;
Best Local Similarity 86.8%; Pred. No. 1.3e-08;
Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 335 LPLEKLRIFRLDVRVSLSAVCRDLFTASNDPLW 372
      |||||
Db 1 LPLEKLRIFRLDVRVSLSAVCHDLLIASNDPLW 38

RESULT 10
US-08-951-621-49
; Sequence 49, Application US/08951621
; Patent No. 6573094
; GENERAL INFORMATION:
; APPLICANT: HARPER, JEFFREY W.
; APPLICANT: ELLEDGE, STEPHEN J.
; TITLE OF INVENTION: F-BOX GENES AND PROTEINS
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/951,621
; FILING DATE: 16-OCT-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: BCM-02999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
US-08-951-621-49

Query Match          6.0%; Score 164; DB 2; Length 38;
Best Local Similarity 86.8%; Pred. No. 1.3e-08;
Matches 33; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 335 LPLEKLRIFRLDVRVSLSAVCRDLFTASNDPLW 372
      |||||
Db 1 LPLEKLRIFRLDVRVSLSAVCHDLLIASNDPLW 38

RESULT 11
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; Sequence 2, Application US/09599287A  
; Patent No. 6635446  
; GENERAL INFORMATION:  
; APPLICANT: Narayanaswamy Ramesh  
; APPLICANT: Ines M. Anton  
; APPLICANT: John H. Hartwig  
; APPLICANT: Raif S. Gena  
; TITLE OF INVENTION: WIP, A WASP-Associated Protein  
; FILE REFERENCE: 1242.1022-004  
; CURRENT APPLICATION NUMBER: US/09/599,287A  
; CURRENT FILING DATE: 2000-06-22  
; PRIOR APPLICATION NUMBER: PCT/US98/27501  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: 60/101,457  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/068,533  
; PRIOR FILING DATE: 1997-12-23  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 503  
; TYPE: PRT  
; ORGANISM: Human  
US-09-599-287A-2

Query Match 4.3%; Score 117.5; DB 2; Length 503;  
Best Local Similarity 33.1%; Pred. No. 0.028; 41; Indels 43; Gaps 9;  
Matches 46; Conservative 9; Mismatches 41; Indels 43; Gaps 9;  
Qy 415 LPSSTHTIPFPYNPLHPPPPSSR-----LPPGIIGGEYDQRTLPYVGDPISSL---IP 466  
Db 294 VPSTPR--PSAPHRPHLRPPPPSRGPPPLPPSSGN--DETPLPQRLNLSLSSSTPLP 349  
Qy 467 GPGET-----PSQFPPLRPRFDP--VGPLPGNPPI-----LPG----- 497  
Db 350 SPGRSGPLPPPSERPPPPVDPDPGRSGPLPPPPVSRNGSTSRALPATQLPSRSGVDS 409  
Qy 498 -RGGNDRF-PFRPSRGRP 514  
Db 410 PRSGRPLPPDRPSAGAP 428

RESULT 15  
US-10-078-547-2  
; Sequence 2, Application US/10078547  
; Patent No. 6927318  
; GENERAL INFORMATION:  
; APPLICANT: Narayanaswamy Ramesh  
; APPLICANT: Miguel A. de la Fuente  
; APPLICANT: Ines M. Anton  
; APPLICANT: Raif S. Gena  
; TITLE OF INVENTION: WIP, A WASP-Associated Protein  
; FILE REFERENCE: 1242.1022-005  
; CURRENT APPLICATION NUMBER: US/10/078,547  
; CURRENT FILING DATE: 2002-02-19  
; PRIOR APPLICATION NUMBER: 09/599,287  
; PRIOR FILING DATE: 2000-06-22  
; PRIOR APPLICATION NUMBER: PCT/US98/27501  
; PRIOR FILING DATE: 1998-12-22  
; PRIOR APPLICATION NUMBER: 60/101,457  
; PRIOR FILING DATE: 1998-09-23  
; PRIOR APPLICATION NUMBER: 60/068,533  
; PRIOR FILING DATE: 1997-12-23  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 503  
; TYPE: PRT  
; ORGANISM: Human  
US-10-078-547-2

Query Match 4.3%; Score 117.5; DB 2; Length 503;  
Best Local Similarity 33.1%; Pred. No. 0.028;

Matches 46; Conservative 9; Mismatches 41; Indels 43; Gaps 9;  
Qy 415 LPSSTHTIPFPYNPLHPPPPSSR-----LPPGIIGGEYDQRTLPYVGDPISSL---IP 466  
Db 294 VPSTPR--PSAPHRPHLRPPPPSRGPPPLPPSSGN--DETPLPQRLNLSLSSSTPLP 349  
Qy 467 GPGET-----PSQFPPLRPRFDP--VGPLPGNPPI-----LPG----- 497  
Db 350 SPGRSGPLPPPSERPPPPVDPDPGRSGPLPPPPVSRNGSTSRALPATQLPSRSGVDS 409  
Qy 498 -RGGNDRF-PFRPSRGRP 514  
Db 410 PRSGRPLPPDRPSAGAP 428

Search completed: February 14, 2006, 21:03:23  
Job time : 47 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 14, 2006, 20:54:48 ; Search time 234 Seconds  
(without alignments)  
1573.871 Million cell updates/sec

Title: US-09-927-458-2  
Perfect score: 2754  
Sequence: 1 MRLVRLKLTWPLEVPETE.....DRFPFRPSRGRTDGRLSFM 522

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2748	99.8	522	1	FBX7_HUMAN	Q9Y311 homo sapien
2	2532	91.9	528	2	Q5TGC3_HUMAN	Q5TGC3 homo sapien
3	2214	80.4	443	2	Q5RBD1_PONPY	Q5RBD1 pongo pygma
4	1984	72.0	522	2	Q68FS3_RAT	Q68fs3 rattus norv
5	1977.5	71.8	523	2	Q8K0A5_MOUSE	Q8K0a5 mus musculu
6	1295	47.0	361	2	Q5Y017_CHICK	Q5y017 gallus gall
7	1261	45.8	399	2	Q5F421_CHICK	Q5f421 gallus gall
8	1247	45.3	233	2	Q5HYB3_HUMAN	Q5hyb3 homo sapien
9	1125	40.8	478	2	Q6DE59_XENLA	Q6de59 xenopus lae
10	1059	38.5	472	2	Q5PQ43_XENLA	Q5pq43 xenopus lae
11	877	31.8	486	2	Q4V8X6_BRARE	Q4v8x6 brachydanio
12	873.5	31.7	483	2	Q5SPK1_BRARE	Q5spk1 brachydanio
13	851.5	30.9	471	2	Q4T8W7_TETNG	Q4t8w7 tetraodon n
14	240.5	8.7	475	2	Q3ZUB8_ARATH	Q3zub8 arabidopsis
15	205	7.4	776	2	Q6GZV6_ORYSA	Q6gzv6 oryza sativ
16	187.5	6.8	350	2	Q3ZUB9_ARATH	Q3zub9 arabidopsis
17	181.5	6.6	1212	2	Q515H3_ENTHI	Q515h3 entamoeba h
18	157	5.7	326	2	Q4S822_DICTDI	Q4s822 dictyosteli
19	147	5.3	270	1	PSMF1_DROME	Q9v637 drosophila
20	145.5	5.3	434	2	Q4W8W0_HUMAN	Q4w8w0 homo sapien
21	145.5	5.3	554	2	Q59EH8_HUMAN	Q59eh8 homo sapien
22	144	5.2	447	1	FBX9_HUMAN	Q9uk97 homo sapien
23	143.5	5.2	271	2	Q5ZJ33_CHICK	Q5zj33 gallus gall
24	140	5.1	435	1	FBX9_RAT	Q5u2l1 rattus norv
25	138.5	5.0	356	2	Q7ZTY2_BRARE	Q7zty2 brachydanio
26	135	4.9	437	1	FBX9_MOUSE	Q9bk06 mus musculu
27	134.5	4.9	1183	2	Q7TSH6_MOUSE	Q7tsh6 mus musculu
28	134.5	4.9	1209	2	Q6PFQ0_MOUSE	Q6pfq0 mus musculu
29	134	4.9	3148	2	Q8H6Q8_PONTR	Q8h6q8 poncirus tr
30	132	4.8	405	2	Q52F83_MAGGR	Q52f83 magnaporthe
31	130.5	4.7	355	2	Q5ZHM6_CHICK	Q5zhm6 gallus gall

32	129.5	4.7	1200	2	Q692P8_MOUSE	Q692p8 mus musculu
33	129	4.7	569	2	Q54CP0_DICTDI	Q54cp0 dictyosteli
34	129	4.7	745	2	Q6Z1Z5_ORYSA	Q6z1z5 oryza sativ
35	128.5	4.7	850	2	O17055-CAEEL	O17055 caenorhabdi
36	127	4.6	579	2	Q4RLQ7_TETNG	Q4rlq7 tetraodon n
37	126.5	4.6	431	2	Q7SY92_XENLA	Q7sy92 xenopus lae
38	126	4.6	355	1	FBX32_HUMAN	Q969p5 homo sapien
39	124.5	4.5	356	2	Q4RFD2_TETNG	Q4rfd2 tetraodon n
40	124.5	4.5	434	2	Q5CD94_CRYHO	Q5cd94 cryptospori
41	124.5	4.5	920	1	21MP7_HUMAN	Q8nrf64 homo sapien
42	124	4.5	980	2	Q60PF6_CAEBR	Q60pf6 caenorhabdi
43	123.5	4.5	1874	2	Q5SBA7_DICTDI	Q5sba7 dictyosteli
44	123.5	4.5	4527	2	Q4RVG0_TETNG	Q4rvgo tetraodon n
45	123	4.5	271	1	PSMF1_HUMAN	Q92530 homo sapien

ALIGNMENTS

RESULT 1  
FBX7\_HUMAN  
ID FBX7\_HUMAN STANDARD; PRT; 522 AA.  
AC Q9Y311; Q5TGC4; Q96HM6; Q9UF21; Q9UKT2;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE F-box only protein 7.  
GN Name=FBX07; Synonym=FBX7;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE OF 41-522, AND VARIANT ILB-115.  
RA MEDLINE=20003060; PubMed=10531035; DOI=10.1016/S0960-9822(00)80020-2;  
RX Cenciarelli C., Chiaur D.S., Guardavaccaro D., Parks W., Vidal M.,  
Pagano M.;  
RT "Identification of a family of human F-box proteins.";  
RL Curr. Biol. 9:1177-1179(1999).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RX MEDLINE=20399565; PubMed=10945468; DOI=10.1006/geno.2000.6211;  
RA Ilyin G.P., Riialand M., Pigeon C., Gugen-Guillouzo C.;  
RT "cDNA cloning and expression analysis of new members of the mammalian  
F-box protein family";  
RL Genomics 67:40-47(2000).  
RN [3]  
RP NUCLEOTIDE SEQUENCE [MRNA].  
RA Collins J.E., Huckle E.J.;  
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
RX PubMed=15461802; DOI=10.1186/gb-2004-5-10-r84;  
RA Collins J.E., Wright C.L., Edwards C.A., Davis M.P., Grinham J.A.,  
Cole C.G., Goward M.E., Aguado B., Malliya M., Mokrab Y., Huckle E.J.,  
Beare D.M., Dunham I.;  
RT "A genome annotation-driven approach to cloning the human ORFeome.";  
RL Genome Biol. 5:RESEARCH84.1-RESEARCH84.11(2004).  
RN [5]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RX MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;  
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,  
Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,  
Begguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,  
Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,  
Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,  
Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,  
Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,  
Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,  
Evans K.L., Fey J.W., Fleming K., French L., Garner A.A.,  
Gilbert J.G.R., Goward M.B., Grahm D.V., Griffiths M.N.D., Hall C.,  
Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,





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RESULT 2
Q5TGC3 HUMAN PRELIMINARY; PRT; 528 AA.
AC Q5TGC3
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE F-box protein 7 (Fragment).
GN Name=FBX07; ORFNames=LL22NC03-28H9.2-002;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Clark G.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
[2]
RP NUCLEOTIDE SEQUENCE.
RA Davies J.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
[3]
RP NUCLEOTIDE SEQUENCE.
RA Smith M.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL035068; CAI19334.1; -; Genomic DNA.
DR EMBL; Z71183; CAI18783.1; -; Genomic DNA.
DR EMBL; AL021937; CAI19588.1; -; Genomic DNA.
DR EMBL; AL021937; CAI19334.1; JOINED; Genomic DNA.
DR EMBL; Z71183; CAI19334.1; JOINED; Genomic DNA.
DR EMBL; AL021937; CAI18783.1; JOINED; Genomic DNA.
DR EMBL; AL035068; CAI18783.1; JOINED; Genomic DNA.
DR EMBL; AL035068; CAI19588.1; JOINED; Genomic DNA.
DR EMBL; Z71183; CAI19588.1; JOINED; Genomic DNA.
DR Ensembl; ENSG00000100225; Homo sapiens.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR SMART; SM00256; FBX; 1.
DR PROSITE; PS50181; FBX; 1.
FT NON TER
SQ SEQUENCE 528 AA; 58298 MW; 467F46F7314E1F86 CRC64;

Query Match 91.9%; Score 2532; DB 2; Length 528;
Best Local Similarity 100.0%; Pred. No. 2.4e-163;
Matches 481; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 SNTFTITLNYKDLPTGDEETLASYGIVSGDLICLLIQDDIPAPNIPSSSTDSEHSSLQNN 101
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Db 48 SNTFTITLNYKDLPTGDEETLASYGIVSGDLICLLIQDDIPAPNIPSSSTDSEHSSLQNN 107
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Qy 102 EQPSLATSSNQTSMQDEQPSDFGQAAQSGVWDDSMLGPSQNFPEAESIQDIAHMAEGT 161
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Db 108 EQPSLATSSNQTSMQDEQPSDFGQAAQSGVWDDSMLGPSQNFPEAESIQDIAHMAEGT 167
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Qy 162 GFYSEPMLCSESVGGVPHSLFTLYQSADCSANDALIIVLHLLMLESGLYIPQTEAKA 221
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Db 168 GFYSEPMLCSESVGGVPHSLFTLYQSADCSANDALIIVLHLLMLESGLYIPQTEAKA 227
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Qy 222 LSMPEKWKLSGVYKLYMHPLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLP 281
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Db 228 LSMPEKWKLSGVYKLYMHPLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLP 287
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Qy 282 ESFTCKEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTQALNLPDVFGLVPLBLKL 341
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Db 288 ESFTCKEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTQALNLPDVFGLVPLBLKL 347
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Qy 342 RIFLLDVRSLVSACRDLFTASNDPLLWRFLYLDRFRDNTVRVQDQDWKELYRKRHI 401
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Db 348 RIFLLDVRSLVSACRDLFTASNDPLLWRFLYLDRFRDNTVRVQDQDWKELYRKRHI 407
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Qy 402 QRKESPKGRFVMLLPSSSTHTIPFPNPLHPRPPSSRLPPGIIIGGEYDQRTPLPVGDPI 461
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|
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Db 408 QRKESPKGRFVMLLPSSSTHTIPFPNPLHPRPPSSRLPPGIIIGGEYDQRTPLPVGDPI 467
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|
|
Qy 462 SSLIPGGEGTSPQFPPLRPDPVGLPGPNPILPGRGGPNDRPFRPSRGRPTDGRLSF 521
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|
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Db 468 SSLIPGGEGTSPQFPPLRPDPVGLPGPNPILPGRGGPNDRPFRPSRGRPTDGRLSF 527
|
|
|
Qy 522 M 522
|
|
|
Db 528 M 528

RESULT 3
Q5RBD1 PONPY PRELIMINARY; PRT; 443 AA.
AC Q5RBD1;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFp469H0739.
GN Name=DKFp469H0739;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RG The German cDNA Consortium;
RA Ottenwaeider B., Obermaier B., Deutschenbaur S., Schaipp A.,
RA Mewes H.W., Weill B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR858720; CAH90929.1; -; mRNA.
DR GO; GO:0006512; P-ubiquitin cycle; IEA.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR SMART; SM00256; FBX; 1.
DR PROSITE; PS50181; FBX; 1.
KW Hypothetical protein.
SQ SEQUENCE 443 AA; 49399 MW; B78AA76A054D3FED CRC64;

Query Match 80.4%; Score 2214; DB 2; Length 443;
Best Local Similarity 97.7%; Pred. No. 7.2e-142;
Matches 421; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 92 DSEHSSIQNNEQPSLATSSNQTSMQDEQPSDFGQAAQSGVWDDSMLGPSQNFPEAESI 151
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|
|
Db 13 DSEHSSIQNNEQPSLATSSNQTSMQDEQPSDFGQAAQSGVWDDSMLGPSQNFPEAESI 72
|
|
|
Qy 152 QDNAHMAEGTGFYSEPMLCSESVGGVPHSLFTLYQSADCSANDALIIVLHLLMLESGL 211
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|
|
Db 73 QDNAHMAEGTGFYSEPMLCSESVGGVPHSLFTLYQSADCSANDALIIVLHLLMLESGL 132
|
|
|
Qy 212 YIPQTEAKALSMPKWKLSGVYKLYMHPLCEGSSATLTCVPLGNLIVVNATLKINNEI 271
|
|
|
Db 133 YIPQTEAKALSMPKWKLSGVYKLYMHPLCEGSSATLTCVPLGNLIVVNATLKINNEI 192
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|
|
Qy 272 RSVKRLQLLPESFTCKEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTQALNLPDVFG 331
|
|
|
Db 193 RSVKRLQLLPESFTCKEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTQALNLPDVFG 252
|
|
|
Qy 332 LVVLPLELKLRIFRLLDVRSLVSACRDLFTASNDPLLWRFLYLDRFRDNTVRVQDQD 391
|
|
|
Db 253 LVVLPLELKLRIFRLLDVRSLVSACRDLFTASNDPLLWRFLYLDRFRDNTVRVQDQD 312
|
|
|
Qy 392 WKELYRKRHIQRKESPKGRFVMLLPSSSTHTIPFPNPLHPRPPSSRLPPGIIIGGEYDQ 451
|
|
|
Db 313 WKELYRKRHIQRKESPKGRFVMLLPSSSTHTIPFPNPLHPRPPSSRLPPGIIIGGEYDQ 372
|
|
|
Qy 452 PTLPVYGDPISSLIIPGGETSPQFPPLRPDPVGLPGPNPILPGRGGPNDRPFRPSR 511
|
|
|
Db 373 PTLPVYGDPISSLIIPGGETSPQFPPLRPDPVGLPGPNPILPGRGGPNDRPFRPSR 432
|
|
|
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[illegible]

```
Db 121 QNEQSDNKAQVEAKQSDRAGSLSEFFSGVLVPEDVDLEEGTGSYPSEPMCLSEADGEI 180
Qy 180 PHSLETLQSDCDANDALIVLIHLMLSEGYIPQGTAKALSMPEKWKLSGVYKLYQM 239
Db 181 PHSLEVLVSABECTSDALIVLHLLMMETGYVPGQTEAKAVSMPEKWRGNGVYKLQYT 240
Qy 240 HPLCEGSSATLTCVPLGNLIVVATLKINNEIRSVKRLQLLPESFICKEKUGENVATYK 299
Db 241 HPLCEGSAGLTCVPLGNLIVVATLKINREIKGVKRIQLLPASVCFQE-PEKVAGYK 299
Qy 300 DLQKLSRLFKDQVYVPLLAFTQALNLPDVFGLVVLPLELKLIRIPELLDVRSLVSACV 359
Db 300 DLQKLSRLFKDQVYVSLAARQAQLNLPDVFGLVVLPLELKLIRIPELLDVRSLVSACV 359
Qy 360 RDLFTASNDPLLRFLYLDRFD 382
Db 360 RDLVAASNDQLLRWPMYLRDRFD 382

RESULT 8
QSHYB3_HUMAN
ID QSHYB3_HUMAN PRELIMINARY; PRT; 233 AA.
AC QSHYB3
DT 10-MAY-2005 (TReMBLrel. 30, Created)
DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
DE Hypothetical protein DKFZp686808113 (fragment).
GN Name=DKFZp686808113;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Fetal kidney;
RG The German cDNA Consortium;
RA Ottenwaelder B., Obermaier B., Deutschenbaur S., Schapp A.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BX648644; CAI46263.1; -; -;
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR SMART; SM00256; FBOX; 1.
DR PROSITE; PS0181; FBOX; 1.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 233 AA; 26616 MW; 39AD4FBB2E64569 CRC64;
Query Match 45.3%; Score 1247; DB 2; Length 233;
Beat Local Similarity 99.6%; Pred. No. 1.3e-76;
Matches 232; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 290 LGENVANYIKDLQKLSRLFKDQVYVPLLAFTQALNLPDVFGLVVLPLELKLIRIPELLDV 349
Db 1 LGENVANYIKDLQKLSRLFKDQVYVPLLAFTQALNLPDVFGLVVLPLELKLIRIPELLDV 60
Qy 350 RSVLSLSAVCRDLFTASNDPLLRFLYLDRFDNDTVRVQDITDWKELYRKRHTQRKESPKG 409
Db 61 RSVLSLSAVCRDLFTASNDPLLRFLYLDRFDNDTVRVQDITDWKELYRKRHTQRKESPKG 120
Qy 410 RVMLLPSSHTTIPYPNPLHPRPFPSSRLPGIIGGYDQRTPTLPYVGDPISLIPGPG 469
Db 121 RVMLLPSSHTTIPYPNPLHPRPFPSSRLPGIIGGYDQRTPTLPYVGDPISLIPGPG 180
Qy 470 ETPSOPPLPRFPDVPGLPGNPILPGRGGNDPRFPSPRGRPTDGRLSFM 522
Db 181 ETPSOPPLPRFPDVPGLPGNPILPGRGGNDPRFPSPRGRPTDGRLSFM 233

RESULT 9
Q6DE59_XENLA
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ID AC Q6DE59_XENLA PRELIMINARY; PRT; 478 AA.
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DE Fbox7-prov protein.
GN Name=fbox7-prov;
OS Xenopus laevis (African clawed frog);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC077283; AAH77283.1; -; mRNA.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001226; Flavodoxin.
DR Pfam; PF00646; F-box; 1.
DR PROSITE; PS0181; FBOX; 1.
DR PROSITE; PS00201; FLAVODOXIN; UNKNOWN 1.
SQ SEQUENCE 478 AA; 53251 MW; 8C12F01E32C1873F CRC64;
Query Match 40.8%; Score 1125; DB 2; Length 478;
Beat Local Similarity 47.5%; Pred. No. 6.7e-68;
Matches 251; Conservative 74; Mismatches 14; Indels 56; Gaps 14;
Qy 1 MRLRVLLKRTWPLEVPEPETEPTLGHLSRLSLCTGWYGSNRTFTTLNKKDLTGDE 60
Db 1 MRLRVVRKQTSRLEAEQPTGLDRLSKLSVTLPSLGSAAETHFTITLNGKDALTEQ 60
Qy 61 ETLASYGIVSGDLICLILOD--DIPAPNIPSSITSEHSLONNEOPSLSATSSNOTSMODE 118
Db 61 TTLESAGIISGDLIVVLLPDSFQAPPAPERD-PRCFLEDPTQP-----CSTANK 111
Qy 119 QPSDSFGQAAQSGVWYNDSDMLGPSQNFESIQDNAHMAEGTGYPSS-EPMLCSSEVGE 177
```

Db 112 RP-----KGADNEGA-----GAMPQAEASPSLDDVAM-EGQLSGPAWEVWMLCSEAVDG 159

Qy 178 QVPHSLETLYQSADCSANDALIVLIHLLMESGYIPOQTEAKALSMPEKWLKSGVYKIQ 237

Db 160 KIPHSLEVLYQTASCSASDADFIVIVHLLMLETGYLHGAETKALCMRDRWSGGAYRLH 219

Qy 238 YHPLCEGSSATLTCVPIGNLVNATUKINNEIRSVKRLQLLPSPFTCKSKLGENVANI 297

Db 220 YTHPLCAVSATVLCPLMGKLVIIINATWKINSEKSVKRLQLLTNSYISYPETONNVASV 279

Qy 298 YKDLQKLSRLFKDQVLYPLLAFTAOALNLPDVGVLVPLLEKLRIFELLDRVRSVLSLSA 357

Db 280 YKDLQKLSGQKQDQVAYPELLAAARQVNLDPDVGVLVPLLEKLRIFELLDIRSLNLISA 339

Qy 358 VCRDLFTASNDPLLRFLYLRDRDNTVRVODTDWKELYRKRHIQRKESPKGRFV---ML 414

Db 340 TKCELLADTDPLLRFLCIRDFRNSLPRLNLTGDKWLYKEFKQKMD--RNRFRVROFL 397

Qy 415 LPSSTHTTIPFPNPLHPRFPSSRLPPGIIGGEVDQRPTLPVVGDPISSLIPGGETPSQ 474

Db 398 PPRNAHPYYPYFN-VFP---PDINYPPIIGGDYDQRPPPIV-----NPTH 440

Qy 475 FPPLRPRDPVGLPGPNPLPGRGPNDRFPFRSGRPTDGRLSFM 522

Db 441 LNP-----FKVTLPPSENDPSIPGSSG-----LRPSRGRGDIRRGFI 478

## RESULT 10

Q5PQ43\_XENLA  
ID Q5PQ43\_XENLA PRELIMINARY; PRT; 472 AA.  
AC Q5PQ43;  
DT 01-FEB-2005 (TrEMBLrel. 29, Created)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)  
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)  
DE LOC495987 protein.  
GN Name=LOC495987;  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
OC Xenopodidae; Xenopus; Xenopus.  
OC NCBI\_TaxID=8355;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Testis;  
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.,  
RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
RT initiative."  
RL Dev. Dyn. 225:384-391(2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Testis;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards D., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Heltón E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzyzinski M.I., Skalek U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "generation and initial analysis of more than 15,000 full-length human  
RT and mouse cdna sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Testis;  
RA Klein S., Gerhard D.S.;  
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC087373; AA087373.1; -, mRNA.  
DR GO; GO:0006512; P:ubiquitin cycle; IEA.  
DR InterPro; IPR001810; P-box.  
DR Pfam; PF00646; P-box; 1.  
DR SMART; SM00256; FBOX; 1.  
DR PROSITE; PS50181; FBOX; 1.  
SQ SEQUENCE 472 AA; 52511 MW; 05EBC51A0D86F7BB CRC64;  
  
Query Match 38 5%; Score 1059; DB 2; Length 472;  
Best Local Similarity 44.2%; Pred. No. 2e-63;  
Matches 234; Conservative 81; Mismatches 150; Indels 64; Gaps 13;  
  
Qy 1 MRLRVRLKRTWPLEVPEPETLGLHLSHLRLSLCTGWYSSNTRFTITLNYKDLPTGDE 60  
Db 1 MRLRVVRKQTRLDLEAEQPTLGDVRSKLSVTLPALGYSAETDFTITLNGKDLTGQ 60  
  
Qy 61 ETLASYGIVSGDLICILQDDIPAPNIPSTSDSEHSLQNNQPSLATSSNQTSMQDEQP 120  
Db 61 TALEAGIISGDLIILLPDS-PIPSPPAPE-----RRDPRCPLEDPTQHCSTALKRP 113  
  
Qy 121 SDSFGQAAQSGYW-NDDSMLGPSQNFESAESIQDNAHMAEGTGFPYS---EPMLCSSEVE 176  
Db 114 KGVNNDGAKAQVRPQTEAAEETSPSMEDVTMET-----PSPAWEVMLCSEAVD 164  
  
Qy 177 GQVPHSLETLYQSADCSANDALIVLIHLLMESGYIPOQTEAKALSMPEKWLKSGVYK 236  
Db 165 GKIPHSLEVLYQTASCSASDADFIVIVHLLMLETGYLQGAESKALCMRDRWSGGAYRL 224  
  
Qy 237 QYHPLCEGSSATLTCVPLGNLVNATUKINNEIRSVKRLQLLPSPFTCKSKLGENVAN 296  
Db 225 HYTHPLCAVSATLACLPMGKLVIN-----DNDPAS 256  
  
Qy 297 IYKDLQKLSRLFKDQVLYPLLAFTAOALNLPDVGVLVPLLEKLRIFELLDRVRSVLSLS 356  
Db 257 YKDLQKLSGQKQDQVAYPELLAAARQVNLDPDVGVLVPLLEKLRIFELLDIRSLNLIS 316  
  
Qy 357 AVCRLDFTASNDPLLRFLYLRDRDNTVRVODTDWKELYRKRHIQRKESPKGRFV---M 413  
Db 317 ATCKELLAAAGDSLSLRFLCIRDFRNSLPRLNLTGDKWLYKEFKQKMD--RNRFRV 374  
  
Qy 414 LPSSTHTTIPFPNPLHPRFPSSRLPPGIIGGEVDQRPTLPVVGDPISSLIPGGETPS 473  
Db 375 LPPRNAHPYYPYFN-IFP---PDFSVYPPGIIGGEVDQRPPPIV-NPTAPPPIGVGPSS 429  
  
Qy 474 QFPPLRPRDPVGLPGPNPLPGRGPNDRFPFRSGRPTDGRLSFM 522  
Db 430 RFSPLSNPFKVTLPFSEEDPSIP---GPRS---LRPSRGRGDIRRGFI 472

## RESULT 11

Q4V8X6\_BRARE  
ID Q4V8X6\_BRARE PRELIMINARY; PRT; 486 AA.  
AC Q4V8X6;  
DT 13-SEP-2005 (TrEMBLrel. 31, Created)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
DE Hypothetical protein LOC558097.  
GN Name=LOC558097;  
OS Brachydanio rerio (zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RT TISSUE=Embryo;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

```
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toehlyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettunen M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Embryo;
RG NIH MGC Project;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC097156; AAH97156.1; -, mRNA.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR SMART; SM00256; FBOX; 1.
DR PROSITE; PS0181; FBOX; 1.
KW Hypothetical protein.
SQ SEQUENCE 486 AA; 53896 MW; 367C5FAD32BB0CC CRC64;

Query Match 31.8%; Score 877; DB 2; Length 486;
Best Local Similarity 39.1%; Pred. No. 4.7e-51;
Matches 212; Conservative 89; Mismatches 165; Indels 76; Gaps 15;

QY 1 MRLVRLKRTWPLEVETETLGHRLSHRLSLCTGWYSSNTFTITLNYKDLPTGDE 60
DB 1 MRLVRLKRTWPLEVETETLGHRLSHRLSLCTGWYSSNTFTITLNYKDLPTGDE 60
QY 61 ETLSYGVISGDLICLIQDDIPAPNIPSSSTDSEHSSLNQNEQPSLATSSNQTSMQ---- 116
DB 61 QSLSCGVVSGDLISVIL-----PA-----SSLEETQTSAAAHQTHTDQAGGS 105
QY 117 DEQSDSPFGQAAGQGVNDDSMGLPSONFAESIQDNA-----HMAEGTGYFSEPMCLC 171
DB 106 HVSSSSVMEQHVQSERV-DQDLLEVRDQOQECVDLQDCMDQOQOQECVCAAPPLLC 164
QY 172 SESVEGVPHSLLETLYQSDACSDANDALIVLHLLMLESYIPQGTAKALSMPEKWKLS 231
DB 165 CEADGLPLALERLDDSTCRSPSDCLMLALHLLLETGFIPOGAVSSGEMPIGWQAA 224
QY 232 -GVYKLYQVHPHLCGSSATLTCVPLGNLIVVNAATKINNEIRSVKRLQLLPESFICKEL 290
DB 225 GGVFLQVHPHLLNSLVSVAVPMGQTLVINAVLKMETSLENSRKLLKLPDEYVTAWT 284
QY 291 GENVANIYKDLQKLSRLFKDQVYPLLAFTQALNLPDVFGVLVPLLEKLIRIFRLDVR 350
DB 285 GGSQGVYRDRLRLSRLVQDLVPLMATAQALGLPLFLGVLPELLLRLLRLLDVR 344
QY 351 SVLSAVCRDLFTASNDPLLRFLYLRDRNTV---RVQDTHKELYRKXHIQKESK 407
DB 345 SVLSAVCRHLNTATHTDASLWRHLLHRLDRFRVSPFAGHQHRTDWRLEYKQYRQKGA 404
QY 408 -KGRFVMLLPSTHTIPFPNPLHPR-PPSS-----RLPPGIIGGEYDQRTLPYVGD 460
DB 405 RGR-----HW--FYPPISLIPFPSSPAPLPYPIIGDYDQMPV----- 446
QY 461 ISSLIPGPGTSPQFPPLPDPVGLPGNPLIPGRGPNDRFPFRSGRPTDGLS 520
DB 447 ---ILP-----RPRFPIGP-----LPGMSAPVGRSLRSPAGSGAADVRA 484
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QY 521 FM 522
DB 485 FI 486

RESULT 12
Q5SPK1_BRARE PRELIMINARY; PRT; 483 AA.
AC Q5SPK1;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Novel protein similar to mouse and human F-box protein 7 (FBXO7).
GN ORFNames=CH211-286M4.2-001;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Phillimore B.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL845512; CAI12002.1; -, Genomic DNA.
DR GO; GO:0006512; P:ubiquitin cycle; IEA.
DR InterPro; IPR001810; F-box.
DR Pfam; PF00646; F-box; 1.
DR SMART; SM00256; FBOX; 1.
DR PROSITE; PS0181; FBOX; 1.
SQ SEQUENCE 483 AA; 53554 MW; 350DB1744D2E05D1 CRC64;

Query Match 31.7%; Score 873.5; DB 2; Length 483;
Best Local Similarity 39.4%; Pred. No. 8.1e-53;
Matches 210; Conservative 90; Mismatches 172; Indels 61; Gaps 14;

QY 1 MRLVRLKRTWPLEVETETLGHRLSHRLSLCTGWYSSNTFTITLNYKDLPTGDE 60
DB 1 MRLVRLKRTWPLEVETETLGHRLSHRLSLCTGWYSSNTFTITLNYKDLPTGDE 60
QY 61 ETLSYGVISGDLICLIQDDIPAPNIPSSSTDSEHSSLNQNEQPSLATSSNQTSMQ---- 116
DB 61 QSLSCGVVSGDLISVIL-----PA-----SSLEETQTSAAAHQTHTDQAGGS 105
QY 117 DEQSDSPFGQAAGQGVNDDSMGLPSONFAESIQDNA-----HMAEGTGYFSEPMCLC 174
DB 106 HVSSSSVMEQHVQSERV-DQDLLEVRDQOQECVDLQDCMDQOQOQECVCAAPPLLC 164
QY 175 VEGQVPHSLLETLYQSDACSDANDALIVLHLLMLESYIPQGTAKALSMPEKWKLS-GV 233
DB 165 EDGLPLALERLDDSTCRSPSDCLMLALHLLLETGFIPOGAVSSGEMPIGWQAGV 224
QY 234 YKLYQVHPHLCGSSATLTCVPLGNLIVVNAATKINNEIRSVKRLQLLPESFICKEL 293
DB 225 FLQVYVHPHLLNSLVSVAVPMGQTLVINAVLKMETSLENSRKLLKLPDEYVTAWT 284
QY 294 VANIKDLQKLSRLFKDQVYPLLAFTQALNLPDVFGVLVPLLEKLIRIFRLDVR 353
DB 285 GGVTRDRLRLSRLVQDLVPLMATAQALGLPLFLGVLPELLLRLLRLLDVR 344
QY 354 SVLSAVCRDLFTASNDPLLRFLYLRDRNTV---RVQDTHKELYRKXHIQKESK-KG 409
DB 345 SVLSAVCRHLNTATHTDASLWRHLLHRLDRFRVSPFAGHQHRTDWRLEYKQYRQKGA 404
QY 410 RVMMLPSTHTIPFPNPLHPRFPSSRLPPIIGGEYDQRTLPYVGDPISSILPGP 469
DB 405 RHWFYPPISLIPF-PSP--PAPLP--LYPPGIIGDYDQMPV-----LIP--- 446
QY 470 ETPSQFPLRPRFDPVGLPGNPLIPGRGPNDRFPFRSGRPTDGLRSLF 522
DB 447 -----RPRFPIGP-----LPGMSAPVGRSLRSPAGSGAADVRAFI 483

RESULT 13
```

Q4T8W7\_TETNG  
ID Q4T8W7\_TETNG PRELIMINARY; PRT; 471 AA.  
AC Q4T8W7;  
DT 13-SEP-2005 (TREMBlrel. 31, Created)  
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)  
DE Chromosome undetermined SCAF7713, whole genome shotgun sequence.  
GN ORFNames=GSTENG0005041001;  
OS Tetraodon nigroviridis (Green puffer).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
OC Tetraontoidea; Tetraodontidae; Tetraodon.  
RN NCBI\_TaxID=99883;  
RP NUCLEOTIDE SEQUENCE.  
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,  
RA Biemont C., Skalli Z., Castolico L., Poulain J., De Berardinis V.,  
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,  
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,  
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,  
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.;  
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
RT the early vertebrate proto-karyotype.";  
RL Nature 431:946-957(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE  
RG Genoscope; Whitehead Institute Centre for Genome Research;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
CC -! CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL: CAAE01007713; CAF90665.1; -: Genomic DNA.  
SQ SEQUENCE 471 AA; 50502 MW; 498364ASCEI31930 CRC64;  
Query Match 30.9%; Score 851.5; DB 2; Length 471;  
Best Local Similarity 38.9%; Pred. No. 2.4e-49;  
Matches 209; Conservative 76; Mismatches 171; Indels 81; Gaps 17;  
QY 1 MRLRVLLKKTWPLEVETETPTGLHLSHLRLSLCTWGSNTRFTITLNYKDLPTGDE 60  
DB 1 MRLRVQVQGKTSLELQGEPRLAELVLLRVVLPVSVGLSAETQFGSLNGSEVLEDTG 60  
QY 61 ETLASYGIVSGDLICLLQDDIPAPNTPSSTDSEHSSLQNEOPLSATSSNOTSMQDEQP 120  
DB 61 QALASCGVSGDLVRVLLD--PAQAAPRAASHQRG-----PAQVATETPASHTEQP 111  
QY 121 SDSFQGAQAGSVNDDSMGLSPQNFPAESIQDNAHMAETGTFYPS-EPMLCSSEVGGV 179  
DB 112 SDHGEAGAP-----AGPAPGWE-----PGWEPMLCSEADAGQA 144  
QY 180 PHSLETYQSADCSNDALIVLHLMESGYIPQGTAKALSMPEKWL-SGVYKLQY 238  
DB 145 PLSLELLFHAQVGGAAVAAAHLLMVETGTPOGCELSADMPAGWRCGGGVRLQY 204  
QY 239 MHPLECGSSATLCTVPLGNLVNATLKINNEIRSVKRLQLLPESFICKLGENVANIY 298  
DB 205 SHRLCGSVVMVAVSGLSALISGLLEVNSQADSVCKLSLEPSSVYTEAMPDGAANA 264  
QY 299 KDLQKLSRLFKDQVYPLLAFTRAQLMLPDVFGVLVPLFLKLRIFLLDVRVLSLSAV 358  
DB 265 KDLKLSRVFKDQVAYPLITASHAMALPEVFGLTALPPELLLRVLLDVRVSLRAAV 324  
QY 359 CRDLFTASNDPLVFLYLRDFR-DNTRVQDDTWKELYKRKHQRKESPKGRFVMLLPS 417  
DB 325 CRHLGAIITSRLALRWHLRYCDRFGSHAGSRDQWKLQYQAVRRQLQPP-----PQ 376

418 STHTIPFP---NP---LHPRPFPSSRLP--PGIIGGEYDQRPTLPYVGDPISSLIPGPG 469  
377 RLH-----YPCLDPRALLHPPF-----FPVPVGIIGGEYDQRSPFP-----G 416  
470 ETPSQFPLPRPDPVGLPLPG-----NPILPGRGPNDRPFPFRSRRPTDGRLSFM 522  
417 PLPQGVLP-RPRYDPMSPFDLDRRPPTISEGAWGCGGARRPG-CGGADVRRGFI 471

RESULT 14  
Q9ZUB8\_ARATH  
ID Q9ZUB8\_ARATH PRELIMINARY; PRT; 475 AA.  
AC Q9ZUB8;  
DT 01-MAY-1999 (TREMBlrel. 10, Created)  
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)  
DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)  
DE F508.33 protein (At1g23780/F508\_31).  
GN Names=F508.33;  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Liu S., Lenz C.,  
RA Li J., Kremenetskaia I., Luros J., Altafi H., Gonzalez A., Araujo R.,  
RA Buehler E., Conn L., Conway A.B., Dunn P., Hansen N., Huizar L.,  
RA Kim C., Palm C.J., Rowley D., Shinn P., Walker M., Davis R.W.,  
RA Ecker J.R., Federspiel N.A., Theologis A.;  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Theologis;  
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,  
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,  
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,  
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,  
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,  
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,  
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,  
RA Ecker J.R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RA Shinn P., Chen H., Cheuk R., Kim C.J., Bowser L., Carninci P.,  
RA Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y.,  
RA Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,  
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,  
RA Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M.,  
RA Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,  
RA Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A.,  
RA Ecker J.R.;  
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AC005990; AAC98033.1; -: Genomic DNA.  
DR EMBL: AY049291; AAK83633.1; -: mRNA.  
DR EMBL: AY149929; AAN31083.1; -: mRNA.  
DR PIR: A86372; A86372.  
DR GO: GO:0006512; Pubiguitin cycle; IEA.  
DR InterPro: IPR001810; F-box.  
DR InterPro: IPR002052; N6\_Mtase.  
DR Pfam: PF00646; F-box; 1.  
DR SMART: SM00256; FBOX; 1.  
DR PROSITE: PS0181; FBOX; 1.  
DR PROSITE: PS00092; N6\_Mtase; UNKNOWN 1.  
SQ SEQUENCE 475 AA; 52947 MW; D068CCFI5448BFC3 CRC64;  
Query Match 8.7%; Score 240.5; DB 2; Length 475;  
Best Local Similarity 24.5%; Pred. No. 7.4e-08;  
Matches 116; Conservative 89; Mismatches 177; Indels 91; Gaps 20;



```
QY 1 MRLRVLLKRTWPLEVPETEPTLGHRLSHRLSLILCTWGYSSNTRFTITLVAKDPL--TG 58
Db 3 LRLRHETRETKLELAAD-TLHDLRRINPTV-----PSSVHLSLNKKDELITPS 53
QY 59 DEETLASYGIVSGDLICILQDDIPAPNIPSPSTDSEHSSLONNQPSLATSSNQTSMODE 118
Db 54 PEDTLRSGLISGDLIYFSL-----AGESSNWKLRDSETVASQSESNTQSVHD- 102
QY 119 QPSDSFOQAAGSGVWNDMSLGPSONFEASIQDNAHMAEG--TGFYPSBPM----- 169
Db 103 --SIGF-----AEVDVVPQAKSNPN-----TSVED-----PEGDISGMEGPEPMDVEQLDM 147
QY 170 --LCSSEVEGQVPHSLET--LYQSADCSANDALIVLIHLMLSEGYI--PQGT----- 218
Db 148 ELAAGSKRLSEPPFLKNILKESGDTSELT-TLALSIVHAWLSEGFVLLNHGSKFNFS 206
QY 219 AKALSMPEKWKLSGVYKLYQMHPKCEGSSATLTCVPLGNLIVVNA TL-----KINNEI-- 271
Db 207 KELLTVSLRYTLPELIKSDNTI---ESVSVKFQNLGFPVVVVYCTVCGSSGRVHMNLDK 263
QY 272 -RSVKRLQLLPESFICKEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTQALNLPDVF 330
Db 264 RRFVPVIDLMDTSTDS---EGSSSIYREVFMFWMVKDRLVIPLLIIGICDKAGLEPPP 320
QY 331 GLVVLPLELKLRIFFELLDVRSVLSLAVCRDLFTASNDPLLWRFLYLRDRDNTYRV--Q 388
Db 321 CLMLRPLELKLILLELFGVSGNMACVCTEMRYLASNDMLWKQCLBEVNFVVTAGD 380
QY 389 DTDWK-----ELYKRHIORKESPGRFVWMLLPSSTHITPF 424
Db 381 SVNWKARFATWROKQLAASDTPFRQNLGRNISTGRSGIRFRIIGDPPF 433

RESULT 15
Q8GZV6 ORYZA
ID Q8GZV6 ORYZA PRELIMINARY; PRT; 776 AA.
AC Q8GZV6
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Hypothetical protein OJ1017C11.10.
GN Name=OJ1017C11.10;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Currie J.,
RA Collura K.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
DR EMBL; AC135157; AA000689.1; -; Genomic_DNA.
DR Gramene; Q8GZV6; -
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0030528; F:transcription regulator activity; IEA.
DR GO; GO:0006464; P:protein modification; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR001810; F-box.
DR InterPro; IPR001092; HLH_basic.
DR InterPro; IPR000209; Pept_S8_S53.
DR InterPro; IPR000626; Ubiquitin.
DR Pfam; PF00646; F-box; 1.
DR Pfam; PF00010; HLH; 1.
DR SMART; SM00256; FBOX; 1.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00213; UBQ; 1.
DR PROSITE; PS01811; FBOX; 1.
DR PROSITE; PS00888; HLH; 1.
DR PROSITE; PS00136; SUBTILASE ASP; UNKNOWN_1.
DR PROSITE; PS50053; UBIQUITIN_2; 1.
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KW Hypothetical protein.
SQ SEQUENCE 776 AA; 83902 MW; F05B3429D2B924BD CRC64;
Query Match 7.4%; Score 205; DB 2; Length 776;
Best Local Similarity 22.0%; Pred. No. 3.8e-05;
Matches 115; Conservative 90; Mismatches 197; Indels 120; Gaps 25;
QY 1 MRLRVLLKRTWPLEVPETEPTLGHRLSHRLSLILCTWGYSSNTRFTITLV 51
Db 1 MKLRLSRMDQGGAGGAAETHRVOLPDT-ATLSVVKAFPLATKLSAAQVPVPAES-VRLTLN 58
QY 52 YKDP-LTGD-BETLASYGIVSGDLICILQDDIPAPNIPSPSTDSEHSSLONN---EQPSL 106
Db 59 RSEELLTPDPSATLPALGLASGDLIYFTL-SPLSPSPPPQPQQAQPLRNPNDVFSI 117
QY 107 ATSSNQTSMDQEQSDSFQQAAGSG---VWDDSMGLGPSONFEASIQDNAHMAEGTG 162
Db 118 AGAADPTKSPVESGSSSSMPQALCTNPGLPVASDPHHPPP-----DVVMAEAF 166
QY 163 FYPSEPMLCSESVGQVPHSLETLYQSAD---CSDANDALIVLIHLMLSEGYI PQGTE 218
Db 167 VIKSK---SSLVGDTKREMNV-GGADGTVIC-----RLVVALLHAALLDAGFLYANPV 216
QY 219 AKALSMPEKWKLSGVY---KLYQMHP-----LCBSSATLTCVPLGNLIVVNA TLKI 267
Db 217 GSCIQLPQNW-ASGSFVPVSMKYTLPELVEALPVVEEGWAVLVNLSLGNFMVVG--HV 273
QY 268 NNEIRSVKRL-----QLLPESFICKEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFT 322
Db 274 PGATSGVRRLLCLELPELAPLLYLDSDVSTAEE---REIHELWRVLKDEMCLPLMISLCQ 330
QY 323 ALNLPDVFGLVVLPLELKLRIFFELLDVRSVLSLAVCRDLFTASNDPLLWRFLYLRDRD 382
Db 331 LNNLSLPPCLMALPGDWAKVLEFVPGVDIARVQCTCKELDRDLAADNMLWKKCEMEF-- 388
QY 383 NTVRVQDT---DWKELY---RK-----RHIQRKESPKGRFVWMLL----- 415
Db 389 NT---QDTGCGMMCKCIYSQDKDVLADKYTCGNYMVKPVTQPGRWLIILVYHSLLCQY 445
QY 416 -----PSSSTHTTIPFYNPPLHPRFPSS 437
Db 446 ITIGLSLLWYHLVDLVQDAPAAAGIHFDCCIIPLPINPYQLPPS 487
```

Search completed: February 14, 2006, 21:01:47  
Job time : 238 secs



GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 14, 2006, 20:54:24 ; Search time 189 Seconds  
(without alignments)  
1213.522 Million cell updates/sec

Title: US-09-927-458-2

Perfect score: 2754

Sequence: 1 MRLVRLKLTWPLEVPETE.....DRFFRPSRGKPTDGRLSFM 522

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_21.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003s.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2748	99.8	522	6	ADA57283 Human sec
2	2748	99.8	522	6	ADA41163 Human sec
3	2748	99.8	522	6	ABR47958 Human sec
4	2748	99.8	522	7	ADC74366 Human sec
5	2744	99.6	522	4	AB35161 Human Skp
6	2744	99.6	522	8	ABM82342 Tumour-as
7	2744	99.6	522	8	ADU46626 Human Fbx
8	2744	99.6	522	9	ADZ70638 Human pro
9	2510	91.1	591	2	AAW68521 Human RIP
10	2489	90.4	482	3	AA83047 F-box pro
11	2489	90.4	482	3	AAO22452 Human F-b
12	2489	90.4	482	9	ADY62371 Human F-b
13	2448.5	88.9	607	4	AAU32109 Novel hum
14	2404	87.3	462	5	ABB90109 Human pol
15	2404	87.3	462	6	ADA57586 Human sec
16	2404	87.3	462	6	ADA41482 Human sec
17	2404	87.3	462	6	ABR48139 Human sec
18	2404	87.3	462	7	ADC74596 Human sec
19	2270	82.4	443	4	AB35160 Human Skp
20	2086.5	75.8	549	4	ABG18510 Novel hum
21	1527	55.4	317	5	ABB90108 Human pol
22	1238	45.0	231	7	ADJ68946 Human hea
23	1086	39.4	221	6	ADA54155 Human pro
24	714	25.9	174	6	ADA57587 Human sec

25	714	25.9	174	6	ADA41483	Ada41483 Human sec
26	714	25.9	174	6	ABR48140	Abz48140 Human sec
27	714	25.9	174	7	ADC74597	Adc74597 Human sec
28	714	25.9	175	2	AA411397	Aay411397 Human sec
29	502	18.2	94	4	AAU32107	Au32107 Novel hum
30	396	14.4	76	8	ABO54274	AbO54274 Human gen
31	299	10.9	113	3	AA87356	Aay87356 Human sig
32	265.5	9.6	225	4	ABG06838	Abg06838 Novel hum
33	264.5	9.6	53	4	ABG18509	Abg18509 Novel hum
34	264.5	9.6	53	4	AAU32108	Au32108 Novel hum
35	249	9.0	47	8	ABO59862	AbO59862 Human gen
36	240.5	8.7	475	3	AA224904	Aa224904 Arabidops
37	215.5	7.8	500	8	ADT59833	Adt59833 Plant pol
38	211	7.7	485	8	ADX97246	Adx97246 Plant ful
39	207	7.5	485	8	ADX96467	Adx96467 Plant ful
40	201	7.3	485	8	ADY05169	Ady05169 Plant ful
41	194	7.0	39	3	AA83054	Ay83054 F-box mot
42	194	7.0	39	5	AAO22459	AaO22459 Human F-b
43	194	7.0	39	9	ADY62378	Ady62378 F-box mot
44	189	6.9	38	2	AA02272	Ay02272 A F-box p
45	189	6.9	38	4	AAE08044	Aae08044 Human F-b

ALIGNMENTS

RESULT 1

ADA57283  
ID ADA57283 standard; protein; 522 AA.  
XX  
AC ADA57283;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Human secreted protein #566.  
XX  
KW immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;  
KW cytosolic; cerebroprotective; neuroprotective; neurotropic;  
KW cardiovascular; antiarteriosclerotic; gene therapy;  
KW human secreted protein; immune disorder; inflammation;  
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;  
KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;  
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;  
KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;  
KW triple helix formation; antisense gene therapy; forensic biology.  
XX  
OS Homo sapiens.  
XX  
FN WO2002102994-A2.  
XX  
PD 27-DEC-2002.  
XX  
PF 19-MAR-2002; 2002WO-US0008278.  
XX  
PR 21-MAR-2001; 2001US-0277340P.  
PR 19-JUL-2001; 2001US-0306171P.  
PR 13-NOV-2001; 2001US-0331287P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Ruben SM;  
XX  
XX WPI; 2003-16751512/16.  
XX  
XX N-PSDB; ADA56387.  
XX  
XX New human secreted polypeptides and polynucleotides, useful for  
XX diagnosing, treating or preventing e.g. immune disorders, inflammatory  
XX conditions, respiratory disorders, cancers, CNS disorders, or  
XX neurodegenerative disorders.  
XX  
XX Claim 13; SEQ ID NO 1473; 1754pp; English.  
XX  
XX The invention relates to 592 new human secreted polypeptides useful for



Best Local Similarity 99.8%; Pred. No. 6.5e-239;  
Matches 521; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRLRVLLKRTWPLEVPEPETEPTLGHLSRLSLCTWGYSSNTRFTITLNYKDPPLTGDE 60  
Db |||||  
Qy 1 MRLRVLLKRTWPLEVPEPETEPTLGHLSRLSLCTWGYSSNTRFTITLNYKDPPLTGDE 60  
Db |||||

Qy 61 ETLASYGIVSGDLICLLIQDDIPAPNIPSSDSEHSSLQNNQPSLATSSNQTSMQDEQP 120  
Db |||||

Qy 61 ETLASYGIVSGDLICLLIQDDIPAPNIPSSDSEHSSLQNNQPSLATSSNQTSMQDEQP 120  
Db |||||

Qy 121 SDSFQQAQSGVWDDSMGLPSONFEAESIQDQNAHMAEGTGYPSPEMLCSEVGEQVP 180  
Db |||||

Qy 121 SDSFQQAQSGVWDDSMGLPSONFEAESIQDQNAHMAEGTGYPSPEMLCSEVGEQVP 180  
Db |||||

Qy 181 HSLETLQYQADCSANDALIVLHLLMESGYIPQTEAKALSMPEKWLKSGVYKQYMH 240  
Db |||||

Qy 181 HSLETLQYQADCSANDALIVLHLLMESGYIPQTEAKALSMPEKWLKSGVYKQYMH 240  
Db |||||

Qy 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQQLPESFICKEKLGENVANIYKD 300  
Db |||||

Qy 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQQLPESFICKEKLGENVANIYKD 300  
Db |||||

Qy 301 LQKLSRLFKDQLVYPLLAFTQALNLPDVGVLVPLELKLIRFLLDVRSLSAVCR 360  
Db |||||

Qy 301 LQKLSRLFKDQLVYPLLAFTQALNLPDVGVLVPLELKLIRFLLDVRSLSAVCR 360  
Db |||||

Qy 361 DLFTASNDPLLRFLYLRDFRDNTVRVQDQTDWKELYRKRHIQRKESPKGRFVMLLPSTH 420  
Db |||||

Qy 361 DLFTASNDPLLRFLYLRDFRDNTVRVQDQTDWKELYRKRHIQRKESPKGRFVMLLPSTH 420  
Db |||||

Qy 421 TIPFPNPLHPRPPSSRLPPGIIGGEYDQRTPLPYVGDPISSLIPIGGETPSQFPPLRP 480  
Db |||||

Qy 421 TIPFPNPLHPRPPSSRLPPGIIGGEYDQRTPLPYVGDPISSLIPIGGETPSQFPPLRP 480  
Db |||||

Qy 481 RFDVPGPLPGNPILPCRGGNDRFPFRPSRGRPTDGRLSFM 522  
Db |||||

Qy 481 RFDVPGPLPGNPILPCRGGNDRFPFRPSRGRPTDGRLSFM 522  
Db |||||

RESULT 3  
ABR47958  
ID ABR47958 standard; protein; 522 AA.  
XX ABR47958;  
AC  
XX  
XX  
DT 12-JUN-2003 (first entry)  
XX  
DE Human secreted protein, SEQ ID 849.  
XX  
XX Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic;  
KW vulnerable; antiinflammatory; neurotropic; neuroprotective;  
KW antiparkinsonian; gene therapy; human; cardiovascular disorder.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO200295010-A2.  
PN  
XX  
XX  
PD 28-NOV-2002.  
XX  
XX 19-MAR-2002; 2002WO-US009785.  
PF  
XX  
XX 21-MAR-2001; 2001US-0277340P.  
PR 19-JUL-2001; 2001US-0306171P.  
PR 13-NOV-2001; 2001US-0331287P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX  
XX Rosen CA, Ruben SM;  
PI  
XX  
XX WPI; 2003-129429/12.  
DR  
XX  
XX Novel human secreted proteins, useful for detecting, preventing,

diagnosing, prognosticating, treating and/or ameliorating cardiovascular disorders such as arrhythmia.

Claim 13; SEQ ID NO 849; 1881pp; English.

The present invention relates to novel human secreted proteins (ABR47633-ABR48145) and their coding sequences (ACC50344-ACC50856). The proteins and their coding sequences are useful for the preparation of a diagnostic or pharmaceutical composition for diagnosing or treating a cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary arteriosclerosis and myocardial ischaemia), neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, pulmonary disorders, renal disorders, proliferative disorders and/or cancerous diseases and conditions, for wound healing and epithelial cell proliferation, to treat inflammation or infection, for treating thrombosis and arteriosclerosis, for treating or preventing neural damage which occurs in neuronal disorders or neurodegenerative conditions such as Alzheimer's disease and Parkinson's disease, to enhance bone and periodontal regeneration and aid in tissue transplants or bone grafts, to prevent skin aging or hair loss, to stimulate growth and differentiation of haematopoietic cells and bone marrow cells when used in combination with other cytokines, to maintain organs before transplantation or for supporting cell culture of primary tissues, to increase or decrease differentiation or proliferation of embryonic stem cells, or to modulate mammalian characteristics or metabolism. Note: The sequence data for this patent was published in electronic format and is available from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)

Seq Sequence 522 AA;

Query Match 99.8%; Score 2748; DB 6; Length 522;  
Best Local Similarity 99.8%; Pred. No. 6.5e-239;  
Matches 521; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRLRVLLKRTWPLEVPEPETEPTLGHLSRLSLCTWGYSSNTRFTITLNYKDPPLTGDE 60  
Db 1 MRLRVLLKRTWPLEVPEPETEPTLGHLSRLSLCTWGYSSNTRFTITLNYKDPPLTGDE 60

Qy 61 ETLASYGIVSGDLICLLIQDDIPAPNIPSSDSEHSSLQNNQPSLATSSNQTSMQDEQP 120  
Db 61 ETLASYGIVSGDLICLLIQDDIPAPNIPSSDSEHSSLQNNQPSLATSSNQTSMQDEQP 120

Qy 121 SDSFQQAQSGVWDDSMGLPSONFEAESIQDQNAHMAEGTGYPSPEMLCSEVGEQVP 180  
Db 121 SDSFQQAQSGVWDDSMGLPSONFEAESIQDQNAHMAEGTGYPSPEMLCSEVGEQVP 180

Qy 181 HSLETLQYQADCSANDALIVLHLLMESGYIPQTEAKALSMPEKWLKSGVYKQYMH 240  
Db 181 HSLETLQYQADCSANDALIVLHLLMESGYIPQTEAKALSMPEKWLKSGVYKQYMH 240

Qy 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQQLPESFICKEKLGENVANIYKD 300  
Db 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQQLPESFICKEKLGENVANIYKD 300

Qy 301 LQKLSRLFKDQLVYPLLAFTQALNLPDVGVLVPLELKLIRFLLDVRSLSAVCR 360  
Db 301 LQKLSRLFKDQLVYPLLAFTQALNLPDVGVLVPLELKLIRFLLDVRSLSAVCR 360

Qy 361 DLFTASNDPLLRFLYLRDFRDNTVRVQDQTDWKELYRKRHIQRKESPKGRFVMLLPSTH 420  
Db 361 DLFTASNDPLLRFLYLRDFRDNTVRVQDQTDWKELYRKRHIQRKESPKGRFVMLLPSTH 420

Qy 421 TIPFPNPLHPRPPSSRLPPGIIGGEYDQRTPLPYVGDPISSLIPIGGETPSQFPPLRP 480  
Db 421 TIPFPNPLHPRPPSSRLPPGIIGGEYDQRTPLPYVGDPISSLIPIGGETPSQFPPLRP 480

Qy 481 RFDVPGPLPGNPILPCRGGNDRFPFRPSRGRPTDGRLSFM 522  
Db 481 RFDVPGPLPGNPILPCRGGNDRFPFRPSRGRPTDGRLSFM 522

RESULT 4

AD74366  
 ID ADC74366 standard; protein; 522 AA.  
 XX  
 AC ADC74366;  
 XX  
 DT 01-JAN-2004 (first entry)  
 XX  
 DE Human secreted protein - SEQ ID 999.  
 XX  
 KW antianaemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;  
 KW antidabetic; immunosuppressive; dermatological; nephrotropic;  
 KW antiparkinsonian; neuroprotective; nootropic; antibacterial; virucide;  
 KW fungicide; antiparasitic; antiarteriosclerotic; vulnerary; cytostatic;  
 KW haemopoietic; haematologic; anaemia; autoimmune disorder;  
 KW rheumatoid arthritis; inflammation; Grave's disease; diabetes;  
 KW systemic lupus erythematosus; glomerulonephritis; neurodegenerative;  
 KW Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;  
 KW cancer; bacterial; viral; fungal; parasitic infection; gene therapy;  
 KW human.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO2003038063-A2.  
 XX  
 PD 08-MAY-2003.  
 XX  
 PF 19-MAR-2002; 2002WO-US008277.  
 XX  
 PR 21-MAR-2001; 2001US-0277340P.  
 PR 19-JUL-2001; 2001US-0306171P.  
 PR 13-NOV-2001; 2001US-0331287P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Ruben SM;  
 XX  
 DR WPI; 2003-430516/40.  
 DR N-PSDB; ADC73751.  
 XX  
 PT New human secreted polypeptide for diagnosing, preventing or treating  
 PT hematopoietic or hematologic disorders (e.g. anemia), autoimmune  
 PT disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or  
 PT atherosclerosis).  
 XX  
 PS Claim 16; SEQ ID NO 999; 2272pp; English.  
 XX  
 CC The invention relates to a novel human secreted polypeptide comprising a  
 CC defined sequence given in the specification. The polypeptide, nucleic  
 CC acid molecule, antibody, agonist or antagonist of the invention may be  
 CC useful for preparing a composition for diagnosing or treating a  
 CC haemopoietic or haematologic disorder such as anaemia, autoimmune  
 CC disorders such as rheumatoid arthritis, inflammation, Grave's disease,  
 CC diabetes, systemic lupus erythematosus or glomerulonephritis,  
 CC neurodegenerative disorders including Parkinson's disease and Alzheimer's  
 CC disease, wounds and hyperproliferative disorders including  
 CC atherosclerosis or cancer, as well as bacterial, viral, fungal or  
 CC parasitic infections. The polypeptide may also be used during gene  
 CC therapy procedures and for identifying a binding partner by contacting  
 CC the polypeptide with a binding partner and determining whether the  
 CC binding partner increases or decreases the activity of the polypeptide.  
 CC The current sequence is that of the human secreted protein of the  
 CC invention.  
 XX  
 SQ Sequence 522 AA;  
 Query Match 99.8%; Score 2748; DB 7; Length 522;  
 Best Local Similarity 99.8%; Pred. No. 6.5e-239;  
 Matches 521; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MRLRVLLKRTWPVPEPTPLGLHRLSHRLSLCTWGYSSNTRFTITLNKDLPTGDE 60  
 DB 1 MRLRVLLKRTWPVPEPTPLGLHRLSHRLSLCTWGYSSNTRFTITLNKDLPTGDE 60

61 ETLASYGIVSGDLICLILODDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNQTSMDQEQP 120  
 61 ETLASYGIVSGDLICLILODDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNQTSMDQEQP 120  
 121 SDSFGQAQSGVWDDSMGLGSPQNFESAESIQDHAHMAEGTGFYPSBMLCSESVGQVP 180  
 121 SDSFGQAQSGVWDDSMGLGSPQNFESAESIQDHAHMAEGTGFYPSBMLCSESVGQVP 180  
 181 HSLETLQSDADCSANDALIVLIHLLMESGYIQGTAKALSMPEKWKLSGVYKLYMH 240  
 181 HSLETLQSDADCSANDALIVLIHLLMESGYIQGTAKALSMPEKWKLSGVYKLYMH 240  
 241 PLCGSSATLTCVPLGNLIVVNATLKNNEIRSVKRLQLLPESFICKELGENVANIYKD 300  
 241 PLCGSSATLTCVPLGNLIVVNATLKNNEIRSVKRLQLLPESFICKELGENVANIYKD 300  
 301 LQKLSRLFKDQLVYPLLAFTQALNLPDVFLGVVLPLELKLRIIRLLDVRSLSAVCR 360  
 301 LQKLSRLFKDQLVYPLLAFTQALNLPDVFLGVVLPLELKLRIIRLLDVRSLSAVCR 360  
 361 DLFTASNDPLLRFLYLRDPRDNTVRVQDITDKELYRKRHIQRKESPKGRFVMLLPSSSTH 420  
 361 DLFTASNDPLLRFLYLRDPRDNTVRVQDITDKELYRKRHIQRKESPKGRFVMLLPSSSTH 420  
 421 TIFYPNPLHPRPPFPSSRLPGIIGGYDQRTPLPYVGDPISSLIIPGETPSQFPPLRP 480  
 421 TIFYPNPLHPRPPFPSSRLPGIIGGYDQRTPLPYVGDPISSLIIPGETPSQFPPLRP 480  
 481 RFDVPGLPGNPILPGRGGNDPRFPRRGRPTDGRLSPM 522  
 481 RFDVPGLPGNPILPGRGGNDPRFPRRGRPTDGRLSPM 522

RESULT 5  
 AAB35161  
 ID AAB35161 standard; protein; 522 AA.  
 XX  
 AC AAB35161;  
 XX  
 DT 09-APR-2001 (first entry)  
 XX  
 DE Human Skpl-associated F-box protein-1 SAF-1beta SEQ ID NO: 10.  
 XX  
 KW Human; protein degradation; siah-mediated degradation protein; SMDP;  
 KW SCP-complex protein; SCP; siah-1alpha; siah-1 interacting protein; SIP;  
 KW Skpl-associated F-box protein; SAF-1; SAF-2; SAD; cancer; cell division;  
 KW Skpl-associated destruction-box protein; inflammatory disease.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200077207-A2.  
 XX  
 PD 21-DEC-2000.  
 XX  
 PF 09-JUN-2000; 2000WO-US015873.  
 XX  
 PR 11-JUN-1999; 99US-00330517.  
 XX  
 PA (BURN-) BURNHAM INST.  
 XX  
 PI Reed JC, Matsuzawa S;  
 XX  
 DR WPI; 2001-071273/08.  
 DR N-PSDB; AAC67285.  
 XX  
 PT Siah-Mediated Degradation Protein, useful for drug screening, for  
 PT therapeutic applications and for functional genomics.  
 XX  
 PS Claim 15; Page 107-108; 121pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences of  
 CC several siah-mediated degradation proteins and SCF-complex proteins.  
 CC These are designated Siah-1alpha, Siah-1 interacting protein (SIP), which

CC encodes two proteins due to alternative splicing (SIP-L and SIP-S), Skpl-  
CC associated F-box protein-1alpha and beta and -2 (SAF-1alpha, SAF-1beta  
CC and SAF-2) and Skpl-associated destruction-box protein (SAD). The  
CC proteins and their coding sequences are useful in the diagnosis and  
CC treatment of cancers, disorders where too little cell division occurs  
CC such as bone marrow aplasia, immunodeficiencies and inflammatory  
CC diseases including sepsis, fibrosis, arthritis and graft versus host  
CC disease  
XX  
XX  
SQ Sequence 522 AA;

Query Match 99.6%; Score 2744; DB 4; Length 522;  
Best Local Similarity 99.6%; Pred. No. 1.5e-238;  
Matches 520; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRLRVLLKRTWPLEVETPTLGLHLSHLRLSLCTGWYSSNTRFTITLNYKDPPLTGDE 60  
Db 1 MRLRVLLKRTWPLEVETPTLGLHLSHLRLSLCTGWYSSNTRFTITLNYKDPPLTGDE 60  
Qy 61 ETLASGIVSGDLICLILQDDIPAPNIPSSSTDSEHSLQNEQPSLATSSNQTSMDQEQ 120  
Db 61 ETLASGIVSGDLICLILQDDIPAPNIPSSSTDSEHSLQNEQPSLATSSNQTSMDQEQ 120  
Qy 121 SDSFGQAQSGVWDDSMGLPSONFEAESIQDNNAHMAEGTGFYPSPEMLCSESVGEQVP 180  
Db 121 SDSFGQAQSGVWDDSMGLPSONFEAESIQDNNAHMAEGTGFYPSPEMLCSESVGEQVP 180  
Qy 181 HSLETLQSAADCSANDALIVLHLLMLESYIPQGTAEAKALSMPEKWLKSGVYKLYMH 240  
Db 181 HSLETLQSAADCSANDALIVLHLLMLESYIPQGTAEAKALSMPEKWLKSGVYKLYMH 240  
Qy 241 PLCEGSSATLTCVPLGNLIVVNAATKINNEIRSVKRLQLLPESFICKEKLGENVANYKD 300  
Db 241 PLCEGSSATLTCVPLGNLIVVNAATKINNEIRSVKRLQLLPESFICKEKLGENVANYKD 300  
Qy 301 LQKLSRLFKDQVYVPLLAFTROALNLPDVGLVPLLEKLRIFRLLDVRSVLSAVCR 360  
Db 301 LQKLSRLFKDQVYVPLLAFTROALNLPDVGLVPLLEKLRIFRLLDVRSVLSAVCR 360  
Qy 361 DLFTASNDPPLLWFLYLRDRFNDTRVQDQDWKELYRKRIHQKESPKGRFVMLLPSSSTH 420  
Db 361 DLFTASNDPPLLWFLYLRDRFNDTRVQDQDWKELYRKRIHQKESPKGRFVMLLPSSSTH 420  
Qy 421 TIFYPNPLHPPSPSSRLPGIIGGYDQRTPLPYVGDPISSLIIPGGETPSQFPPLRP 480  
Db 421 TIFYPNPLHPPSPSSRLPGIIGGYDQRTPLPYVGDPISSLIIPGGETPSQFPPLRP 480  
Qy 481 RFDVGLPGNPILPGRGPNDRFPFRPSGRPTDGRLSFM 522  
Db 481 RFDVGLPGNPILPGRGPNDRFPFRPSGRPTDGRLSFM 522

RESULT 6  
ABM82342  
ID ABM82342 standard; protein; 522 AA.  
AC ABM82342;  
XX  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Tumour-associated antigenic target (TAT) polypeptide PR083271, SEQ:6018.  
XX  
XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;  
KW tumour; diagnosis; cell proliferative disorder; breast cancer;  
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;  
KW central nervous system cancer; bladder cancer; pancreatic cancer;  
KW cervical cancer; melanoma; leukaemia; hybridisation probe;  
KW chromosome identification; chromosome mapping; gene mapping;  
KW gene therapy; cytostatic.  
XX  
XX Homo sapiens.  
XX  
XX WO2004030615-A2.

XX 15-APR-2004.  
XX 29-SEP-2003; 2003WO-US028547.  
XX 02-OCT-2002; 2002US-0414971P.  
XX (GETH ) GENENTECH INC.  
XX Wu TD, Zhang Z, Zhou Y;  
XX WPI; 2004-347921/32.  
XX N-PSDB; ACN40919.  
XX  
XX New tumor-associated antigenic target polypeptides and nucleic acids,  
XX useful in preparing a medicament for treating or detecting a  
XX proliferative disorder, e.g. breast, lung, colorectal, ovarian or  
XX prostate cancer or tumor.  
XX  
XX Claim 12; SEQ ID NO 6018; 7273pp; English.  
XX  
XX The invention relates to human tumour-associated antigenic target (TAT)  
XX polypeptides, and their related nucleic acids. The TAT polypeptides are  
XX overexpressed in cancer tissues compared to normal tissues, and may thus  
XX serve as effective targets for the diagnosis and treatment of cancer in  
XX mammals. The invention also relates to nucleic acid and polypeptide  
XX sequences at least 80% identical to the TAT nucleic acids and  
XX polypeptides; expression vectors and host cells comprising a TAT nucleic  
XX acid; an antibody specific for a TAT polypeptide; a peptide or organic  
XX molecule which binds to a TAT polypeptide; fusion proteins comprising a  
XX TAT polypeptide; and methods and compositions for the treatment or  
XX diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,  
XX antibodies, antagonists, binding molecules and compositions are useful  
XX for diagnosing or treating a cell proliferative disorder associated with  
XX increased TAT expression, particularly cancers such as breast cancer,  
XX colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder  
XX cancer, pancreatic cancer, cervical cancer, cancers of the central  
XX nervous system, melanoma and leukaemia. TAT nucleic acids may further be  
XX used as hybridisation probes, in chromosome and gene mapping, in  
XX chromosome identification and in gene therapy. The present sequence  
XX represents a TAT polypeptide of the invention  
XX  
XX Sequence 522 AA;

Query Match 99.6%; Score 2744; DB 8; Length 522;  
Best Local Similarity 99.6%; Pred. No. 1.5e-238;  
Matches 520; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRLRVLLKRTWPLEVETPTLGLHLSHLRLSLCTGWYSSNTRFTITLNYKDPPLTGDE 60  
Db 1 MRLRVLLKRTWPLEVETPTLGLHLSHLRLSLCTGWYSSNTRFTITLNYKDPPLTGDE 60  
Qy 61 ETLASGIVSGDLICLILQDDIPAPNIPSSSTDSEHSLQNEQPSLATSSNQTSMDQEQ 120  
Db 61 ETLASGIVSGDLICLILQDDIPAPNIPSSSTDSEHSLQNEQPSLATSSNQTSMDQEQ 120  
Qy 121 SDSFGQAQSGVWDDSMGLPSONFEAESIQDNNAHMAEGTGFYPSPEMLCSESVGEQVP 180  
Db 121 SDSFGQAQSGVWDDSMGLPSONFEAESIQDNNAHMAEGTGFYPSPEMLCSESVGEQVP 180  
Qy 181 HSLETLQSAADCSANDALIVLHLLMLESYIPQGTAEAKALSMPEKWLKSGVYKLYMH 240  
Db 181 HSLETLQSAADCSANDALIVLHLLMLESYIPQGTAEAKALSMPEKWLKSGVYKLYMH 240  
Qy 241 PLCEGSSATLTCVPLGNLIVVNAATKINNEIRSVKRLQLLPESFICKEKLGENVANYKD 300  
Db 241 PLCEGSSATLTCVPLGNLIVVNAATKINNEIRSVKRLQLLPESFICKEKLGENVANYKD 300  
Qy 301 LQKLSRLFKDQVYVPLLAFTROALNLPDVGLVPLLEKLRIFRLLDVRSVLSAVCR 360  
Db 301 LQKLSRLFKDQVYVPLLAFTROALNLPDVGLVPLLEKLRIFRLLDVRSVLSAVCR 360  
Qy 361 DLFTASNDPPLLWFLYLRDRFNDTRVQDQDWKELYRKRIHQKESPKGRFVMLLPSSSTH 420

Db 361 DLFTASNDPLLRFLYLRDFDNTVRVQDITDKELYRKRHIQRKESPKGRFVMLLPSSSTH 420  
Qy 421 TIPYPNPLHRRPFPSSRLPGIIGGEYDQRPTLPYVGDPISSLIPIGGETPSQFPPLRP 480  
Db 421 TIPYPNPLHRRPFPSSRLPGIIGGEYDQRPTLPYVGDPISSLIPIGGETPSQFPPLRP 480  
Qy 481 RFDVPGLPGNPILPGRGNDPFPFPSPGRPTDGLSPM 522  
Db 481 RFDVPGLPGNPILPGRGNDPFPFPSPGRPTDGLSPM 522

RESULT 7  
ADU46626  
ID ADU46626 standard; protein; 522 AA.  
XX  
AC ADU46626;  
XX  
DT 27-JAN-2005 (first entry)  
XX  
DE Human Fbx7 protein sequence.

KW Fbx7; cancer; cyclin-D; proto oncogene; cdk6; cell cycle;  
KW E3 ubiquitin ligase; SCF; F box; lung cancer; Fbx7 inhibitor;  
KW colon cancer; hematological cancer; leukaemia; lymphoma; sarcoma;  
KW carcinoma; adenocarcinoma; head and neck cancer; parathyroid adenoma;  
KW oncoprotein; gene therapy; cytostatic; anti-cancer.  
XX  
OS Homo sapiens.

XX Key Location/Qualifiers  
FH Domain 129..169  
FT /note = Non-contiguous domain in Fbx7. Known to interact  
FT with cdk6  
FT Region 335..372  
FT /note = "F box motif"  
FT Domain 398..522  
FT /note = Non-contiguous domain in Fbx7. Known to interact  
FT with cdk6  
FT /label = Proline\_Rich\_domain  
FT Region 406  
FT /note = "Cyclin/cdk serine phosphodiester site"

PN WO2004093919-A2.  
XX  
XX 04-NOV-2004.  
XX  
XX 22-APR-2004; 2004WO-GB001743.  
XX  
XX 22-APR-2003; 2003GB-00009116.  
XX  
XX (UNLO ) UNIV COLLEGE LONDON.  
XX  
XX Laman H;  
XX  
XX WPI; 2004-775870/76.  
XX  
XX N-PSDB; ADU46625.  
XX  
XX Use of an inhibitor of Fbx7 in the manufacture of a medicament for  
XX treating cancer, such as lung cancer, colon cancer or a hematological  
XX cancer, or in drug screening purposes.  
XX  
XX Disclosure; SEQ ID NO 2; 69pp; English.

XX The patent discloses inhibitor of Fbx7 in the manufacture of a medicament  
XX for use on the treatment of cancer. D-type cyclins are considered as  
XX proto oncogenes, the over expression of these cyclins activates the G1  
XX kinases, cdk4 and cdk6 proteins. These in turn activate the  
XX retinoblastoma protein, permitting entry into the cell cycle. Fbx7  
XX distinguishes between the G1 cdk6 and specifically enhances the levels of  
XX cyclin/cdk6 complexes. The protein abundance in a cell is regulated both  
XX at the level of rates of synthesis and of degradation. Poly-  
XX ubiquitination mediated degradation is mediated via the E3 ubiquitin

CC ligases. The best characterised E3 activities include the anaphase-  
CC promoting complex (APC), the HECT domain proteins, and the SCF complexes.  
CC SCF E3 ubiquitin ligase comprises of multiple subunits, including Skp1, a  
CC cullin protein, a RING finger protein, and a F box motif, which binds the  
CC skp1 subunit. In humans, two Fbx proteins skp2 and cdc4 have been  
CC identified as being critical for the turnover of important cell cycle  
CC regulators, p27, and cyclin E. It has been observed that cells engineered  
CC to express Fbx7, become transformed, and exhibit phenotypes of a cancer  
CC cell. Fbx7 over expression has been observed in lung cancer, colon cancer  
CC and hematological cancers. Thus, Fbx7 is a novel oncoprotein which acts  
CC by way of cyclins/cdk6. Thus Fbx inhibitors of the invention can be used  
CC to treat cancers such as leukaemia, lymphoma, sarcoma, carcinoma,  
CC adenocarcinoma, head and neck cancer, parathyroid adenoma. The invention  
CC also related to a pharmaceutical composition comprising the Fbx7, for  
CC treating a host suffering from cancer. The inhibitor may be a chemical  
CC small molecule or can be an antisense RNA, inhibiting the Fbx7 expression  
CC by RNA interference (RNAi). The objective of using the inhibitor would be  
CC to, inhibit Fbx7 in the interaction between Fbx7 and a D-type cyclin  
CC and/or cdk6 in the host. The sequence presented here is the human Fbx7  
CC protein sequence.  
XX  
XX Sequence 522 AA;

Query Match 99.6%; Score 2744; DB 8; Length 522;  
Best Local Similarity 99.6%; Pred. No. 1.5e-238;  
Matches 520; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRLRVLLKRTWPLEVPEPETETLGHLSRLSLCTLTGWYSSNTRFTITLNYKDLTDE 60  
Db 1 MRLRVLLKRTWPLEVPEPETETLGHLSRLSLCTLTGWYSSNTRFTITLNYKDLTDE 60  
Qy 61 ETLASYGIVSGDLICLLIQDDIPAPNIPSSDSSHSSIQNNEQPSLATSSNQTSMQDSQP 120  
Db 61 ETLASYGIVSGDLICLLIQDDIPAPNIPSSDSSHSSIQNNEQPSLATSSNQTSLQDSQP 120  
Qy 121 SDSFQGAAGVWVNDSDMLGPSQNFEAESIQDNHMAEGTFYSEPMLCSESVGEQVP 180  
Db 121 SDSFQGAAGVWVNDSDMLGPSQNFEAESIQDNHMAEGTFYSEPMLCSESVGEQVP 180  
Qy 181 HSLETLQSDADCSANDALIVLIHLLMESGYIPQGTAKALSMPKWKLSGVYKLOVMH 240  
Db 181 HSLETLQSDADCSANDALIVLIHLLMESGYIPQGTAKALSMPKWKLSGVYKLOVMH 240  
Qy 241 PLCEGSSATLTCPVLGNLIVVNATLKINNEIRSVKRLQLLPESFICKKLGENVANIYKD 300  
Db 241 PLCEGSSATLTCPVLGNLIVVNATLKINNEIRSVKRLQLLPESFICKKLGENVANIYKD 300  
Qy 301 LQKLSRLFKDOLVYPLLAFTQALNLPDVFGVLVPLLELKLRIFRLLDVRSVLSAYCR 360  
Db 301 LQKLSRLFKDOLVYPLLAFTQALNLPDVFGVLVPLLELKLRIFRLLDVRSVLSAYCR 360  
Qy 361 DLFTASNDPLLRFLYLRDFDNTVRVQDITDKELYRKRHIQRKESPKGRFVMLLPSSSTH 420  
Db 361 DLFTASNDPLLRFLYLRDFDNTVRVQDITDKELYRKRHIQRKESPKGRFVMLLPSSSTH 420  
Qy 421 TIPYPNPLHRRPFPSSRLPGIIGGEYDQRPTLPYVGDPISSLIPIGGETPSQFPPLRP 480  
Db 421 TIPYPNPLHRRPFPSSRLPGIIGGEYDQRPTLPYVGDPISSLIPIGGETPSQFPPLRP 480  
Qy 481 RFDVPGLPGNPILPGRGNDPFPFPSPGRPTDGLSPM 522  
Db 481 RFDVPGLPGNPILPGRGNDPFPFPSPGRPTDGLSPM 522

RESULT 8  
ADZ70638  
ID ADZ70638 standard; protein; 522 AA.  
XX  
AC ADZ70638;  
XX  
DT 30-JUN-2005 (first entry)  
XX  
DE Human protein from lung cancer marker gene FBX07.

XX Tumor marker; lung tumor; cytostatic; neoplasm; expression;  
 KW DNA microarray.  
 XX  
 XX Homo sapiens.  
 XX WO2005032495-A2.  
 XX 14-APR-2005.  
 XX 01-OCT-2004; 2004WO-US034163.  
 XX 03-OCT-2003; 2003US-0508355P.  
 XX (FARB ) BAYER PHARM CORP.  
 XX Taylor I, Pauloski NR, Bigwood D;  
 XX WPI; 2005-285325/29.  
 XX N-PSDB; ADZ70637.  
 XX  
 XX Providing a patient diagnosis for lung cancer comprises comparing the  
 PT level of expression of genes or gene products in a biological sample from  
 PT the patient with that from a normal individual.  
 XX  
 XX Claim 3; SEQ ID NO 323; 60pp; English.  
 XX  
 XX The invention relates to providing a patient diagnosis for lung cancer  
 CC comprising comparing the level of expression of genes or gene products in  
 CC a biological sample from the patient with the level of expression of  
 CC genes or gene products in a biological sample from a normal individual.  
 CC Also included are distinguishing between normal and disease tissues,  
 CC monitoring the response of a patient being treated for lung cancer by  
 CC administering an anti-cancer agent, identifying a compound useful for the  
 CC treatment of lung cancer and an array for distinguishing between normal  
 CC and disease tissues (comprising 2 or more probes corresponding to 2 or  
 CC more genes selected from any of the 200 nucleotide sequences given in the  
 CC specification, or 2 or more polypeptides comprising any of the 200 amino  
 CC acid sequences given in the specification). In providing a patient  
 CC diagnosis for lung cancer, one or more genes are selected from any of the  
 CC 200 nucleotide sequences as mentioned in the specification, or one or  
 CC more gene products are polypeptides selected from any of the 20 amino  
 CC acid sequences mentioned in the specification. The methods are useful for  
 CC detecting and treating lung cancer. These may also be used for designing,  
 CC identifying and optimizing therapeutics for cancer. The present sequence  
 CC represents a protein from one of the 200 lung cancer marker genes. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 XX Sequence 522 AA;

Query Match 99.6%; Score 2744; DB 9; Length 522;  
 Best Local Similarity 99.6%; Pred. No. 1.5e-238;  
 Matches 520; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLRLVRLKRTWPLEVETETPTLGLHSLRLSLCTWTGYSNTRFTITLNYKDLPTGDE 60  
 DB 1 MLRLVRLKRTWPLEVETETPTLGLHSLRLSLCTWTGYSNTRFTITLNYKDLPTGDE 60  
 QY 61 ETLASYGIVSGDLICLILQDDIPAPNIPSTDSHSLQNNQPSLATSNQTSMDQEQP 120  
 DB 61 ETLASYGIVSGDLICLILQDDIPAPNIPSTDSHSLQNNQPSLATSNQTSMDQEQP 120  
 QY 121 SDSFQGAAGVWDDSMGLPSONFEASIQDNAHMAETGTFPSPMLCSSEVEQVP 180  
 DB 121 SDSFQGAAGVWDDSMGLPSONFEASIQDNAHMAETGTFPSPMLCSSEVEQVP 180  
 QY 181 HSLETLYQSADCSANDALIVLHLLMESGYIPQGTAKALSMPEKWKLSGVYKQYMH 240  
 DB 181 HSLETLYQSADCSANDALIVLHLLMESGYIPQGTAKALSMPEKWKLSGVYKQYMH 240  
 QY 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKELGENVANIYKD 300

Db 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKELGENVANIYKD 300  
 QY 301 LOKLSRLFKDQLVYPLLAFTQALNLPDVGLVVLPLELKLRIFRLLDVRVLSVACR 360  
 Db 301 LOKLSRLFKDQLVYPLLAFTQALNLPDVGLVVLPLELKLRIFRLLDVRVLSVACR 360  
 QY 361 DLFTASNDPLLMRFYLRLDFRDNTVRVQDITDMKELYRKRHIQRKESPKGRFVMLLPSSSTH 420  
 Db 361 DLFTASNDPLLMRFYLRLDFRDNTVRVQDITDMKELYRKRHIQRKESPKGRFVMLLPSSSTH 420  
 QY 421 TIIFYPNPLHPRPPSSRLPPGIIGGYDQRPPLPYVGDPISSLIPOGETPSPQPPPLRP 480  
 Db 421 TIIFYPNPLHPRPPSSRLPPGIIGGYDQRPPLPYVGDPISSLIPOGETPSPQPPPLRP 480  
 QY 481 RFDVVGPLPGPNPILPGRGGPNDRFPFRPSRGRPTDGRLSFM 522  
 Db 481 RFDVVGPLPGPNPILPGRGGPNDRFPFRPSRGRPTDGRLSFM 522

## RESULT 9

AAW68521  
 ID AAW68521 standard; protein; 591 AA.

XX  
 AC AAW68521;

XX 25-JAN-1999 (first entry)

XX Human RIP-associated protein.

XX Human; RIP-associated protein; RAP; primer; PCR; amplification; probe;  
 KW hybridisation; death domain; MORT MODULE; ICE-like family protease;  
 KW kinase; TRAF domain; inflammation; cell death; tumour; HIV; infection.  
 XX Homo sapiens.

XX WO9841624-A1.

XX 24-SEP-1998.

XX 19-MAR-1998; 98WO-IL000125.

XX 19-MAR-1997; 97IL-00120485.

XX (YEDA ) YEDA RES & DEV CO LTD.

PI Wallach D, Kovalenko A;

XX WPI; 1998-531565/45.

XX N-PSDB; AAV57200.

XX DNA encoding RIP-associated protein (RAP) - useful for, e.g. treatment of  
 PT tumour cells or HIV-infected cells.

XX Claim 10; Fig 2; 65pp; English.

XX This sequence represent part of a human RIP-associated protein (RAP). The  
 CC coding sequence was isolated from a B-cell library by a yeast 2-hybrid  
 CC screen using the RIP protein devoid of its "death domain" as a bait. The  
 CC screen isolated a clone of about 1.9 kb. Primers were generated based on  
 CC the sequence and used to PCR amplify probes for screening a colon and  
 CC heart cDNA library. A further 300 bp of sequence was determined, which  
 CC was added to the 1.9 kb of sequence from the B-cell library. The encoded  
 CC protein does not contain a "death domain", MORT MODULE, ICE-like family  
 CC protease domain, kinase domain, nor TRAF domains. RAP was shown to bind  
 CC only to RIP and not to TRADD, MORT-1, p55-R, p75-R or MACH. The protein  
 CC can be used to modulate or mediate RIP modulated/mediated intracellular  
 CC effects on the inflammation, cell death or cell survival pathways in  
 CC which RIP is involved, e.g. for treating tumour cells or HIV-infected  
 CC cells

XX Sequence 591 AA;

SQ



Query Match	91.1%; Score 2510; DB 2; Length 591;	
Best Local Similarity	99.6%; Pred. No. 2.5e-217;	
Matches 479; Conservative	0; Mismatches	0; Indels 2; Gaps 1;
Qy	42	SNTRFTITLNYKDPDLTGDEETLASVIGVSGDLICLIILQDDIPAPNIPSTDSHSSLQNN 101
Db	113	SNTRFTITLNYKDPDLTGDEETLASVIGVSGDLICLIILQDDIPAPNIPSTDSHSSLQNN 172
Qy	102	EQPSLATSSNOTSMODEQPSDFOGAAQSGVWDDSMLGPSQNFPEASIQDNAMHABGT 161
Db	173	EQ--LATSSNOTSMODEQPSDFOGAAQSGVWDDSMLGPSQNFPEASIQDNAMHABGT 230
Qy	162	GFYSEPMCLCSVEGVQPHSLETLYQSDADCDANDALIIVLIHLLMLESYVPOGTEAKA 221
Db	231	GFYSEPMCLCSVEGVQPHSLETLYQSDADCDANDALIIVLIHLLMLESYVPOGTEAKA 290
Qy	222	LSMPEKWKLSGVYKLYQVHPLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLP 281
Db	291	LSMPEKWKLSGVYKLYQVHPLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLP 350
Qy	282	ESFICKEKLGENVANIYKDLQKLSRLFKDQVYPLLAFTROALNLPDVFGVLVPLELKL 341
Db	351	ESFICKEKLGENVANIYKDLQKLSRLFKDQVYPLLAFTROALNLPDVFGVLVPLELKL 410
Qy	342	RIFRLDVRSVLSAVCRDLFTASNDPDLWRFLYLRDRFRDNTVRVQDWDKELYRKHHI 401
Db	411	RIFRLDVRSVLSAVCRDLFTASNDPDLWRFLYLRDRFRDNTVRVQDWDKELYRKHHI 470
Qy	402	QRKESPKGRFVWLLPSSSTHTTIPFPNPLHPRFPSSRLPPGIIGEYDQRTPLPVGDPI 461
Db	471	QRKESPKGRFVWLLPSSSTHTTIPFPNPLHPRFPSSRLPPGIIGEYDQRTPLPVGDPI 530
Qy	462	SSLIPGGETSPQFPPLRPDPVGPLPGPNPILPGRGGPNDRPFRPSRGRPTDGRLSF 521
Db	531	SSLIPGGETSPQFPPLRPDPVGPLPGPNPILPGRGGPNDRPFRPSRGRPTDGRLSF 590
Qy	522	M 522
Db	591	M 591
RESULT 10		
AA083047	AA083047 standard; protein; 482 AA.	
XX	AC	AA083047;
XX	DT	16-AUG-2000 (first entry)
XX	DE	F-box protein FBP-7.
XX	KW	F-box protein; FBP; diagnosis; treatment; screening; agonist; antagonist;
XX	KW	proliferative disorder; differentiative disorder; breast cancer;
XX	KW	prostate cancer; ovarian cancer; cancer; small cell lung carcinoma;
XX	KW	immune disorder; cardiovascular disorder; inflammatory disorder; human.
XX	OS	Homo sapiens.
XX	PN	WO200012679-A1.
XX	PD	09-MAR-2000.
XX	PF	27-AUG-1999; 99WO-US019560.
XX	PR	28-AUG-1998; 98US-0098355P.
XX	PR	03-FEB-1999; 99US-0118568P.
XX	PR	15-MAR-1999; 99US-0124449P.
XX	PA	(UUNY ) UNIV NEW YORK STATE.
XX	PI	Chiaur DS, Pagano M, Latres E;
XX	PI	WPI; 2000-256635/22.
DR	N-PSDB; AA293356.	
XX	Novel nucleic acid for screening compounds useful for treating	
PT	proliferative and differentiative disorders such as cancer and immune	
PT	disorders comprises sequences encoding ubiquitin ligases.	
XX	Claim 10; Fig 10a; 245pp; English.	
XX	Nucleic acids encoding substrate-targeting subunits of ubiquitin ligases	
CC	with F-box motifs (F-box proteins) are useful for diagnosis of	
CC	proliferative and differentiated related disorders by measuring FBP gene	
CC	expression. Cells expressing such proteins or their fragments are useful	
CC	for screening compounds. The compounds are agonists or antagonists, which	
CC	are useful for treating a proliferative or differentiative disorder in a	
CC	mammal such as breast, ovarian and prostate cancer and small cell lung	
CC	carcinoma and also major opportunistic infections, immune disorders,	
CC	cardiovascular diseases and inflammatory disorders. FBP protein, analogs,	
CC	derivatives and their subsequences, anti-FBP antibodies are also useful	
CC	in diagnosis of the disorders	
XX	Sequence 482 AA;	
Qy	Query Match	90.4%; Score 2489; DB 3; Length 482;
Db	Best Local Similarity	98.1%; Pred. No. 1.5e-215;
Qy	Matches 472; Conservative	5; Mismatches 4; Indels 0; Gaps 0;
Qy	42	SNTRFTITLNYKDPDLTGDEETLASVIGVSGDLICLIILQDDIPAPNIPSTDSHSSLQNN 101
Db	2	SNTRFTITLNYKDPDLTGDEETLASVIGVSGDLICLIILQDDIPAPNIPSTDSHSSLQNN 61
Qy	102	EQPSLATSSNOTSMODEQPSDFOGAAQSGVWDDSMLGPSQNFPEASIQDNAMHABGT 161
Db	62	EQPSLATSSNOTSIQDEQPSDFOGAAQSGVWDDSMLGPSQNFPEASIQDNAMHABGT 121
Qy	162	GFYSEPMCLCSVEGVQPHSLETLYQSDADCDANDALIIVLIHLLMLESYVPOGTEAKA 221
Db	122	GFYSEPMCLCSVEGVQPHSLETLYQSDADCDANDALIIVLIHLLMLESYVPOGTEAKA 181
Qy	222	LSMPEKWKLSGVYKLYQVHPLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLP 281
Db	182	LSLPERKWKLSGVYKLYQVHPLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLP 241
Qy	282	ESFICKEKLGENVANIYKDLQKLSRLFKDQVYPLLAFTROALNLPDVFGVLVPLELKL 341
Db	242	ESFICKEKLGENVANIYKDLQKLSRLFKDQVYPLLAFTROALNLPDVFGVLVPLELKL 301
Qy	342	RIFRLDVRSVLSAVCRDLFTASNDPDLWRFLYLRDRFRDNTVRVQDWDKELYRKHHI 401
Db	302	RIFRLDVRSVLSAVCRDLFTASNDPDLWRFLYLRDRFRDNTVRVQDWDKELYRKHHI 361
Qy	402	QRKESPKGRFVWLLPSSSTHTTIPFPNPLHPRFPSSRLPPGIIGEYDQRTPLPVGDPI 461
Db	362	QRKESPKGRFVWLLPSSSTHTTIPFPNPLHPRFPSSRLPPGIIGEYDQRTPLPVGDPI 421
Qy	462	SSLIPGGETSPQFPPLRPDPVGPLPGPNPILPGRGGPNDRPFRPSRGRPTDGRLSF 521
Db	422	SSLIPGGETSPQFPPLRPDPVGPLPGPNPILPGRGGPNDRPFRPSRGRPTDGRLSF 481
Qy	522	M 522
Db	482	M 482
RESULT 11		
AA022452	AA022452 standard; protein; 482 AA.	
XX	AC	AA022452;
XX	DT	11-OCT-2002 (first entry)
XX	DE	Human F-box protein FBP7 SEQ ID No 14.





and comparing the level of FBPI expression or activity in the affected individual with the level of FBPI expression or activity in a clinically normal individual, such that if decreased levels of FBPI expression or activity are detected in the affected individual relative to the clinically normal individual, an FBPI-related infertility disorder is diagnosed, (ii) a pharmaceutical composition for the treatment of FBPI-related infertility, comprising a compound that modulates FBPI activity and a carrier, (iii) a method of treating (M3) FBPI-related infertility by administering to an individual in the need of such treatment a compound that modulates FBPI activity, in an amount effective for the treatment of the infertility, and (iv) a method of detecting (M4) an FBPI infertility disorder in a mammal by measuring the level of FBPI activity or expression in the mammal, such that if the measured FBPI activity or expression differs from the level found in clinically normal individuals, then a FBPI-related infertility disorder is detected. Method (M1) is useful for screening compounds that modulate FBPI-related disorders and are useful for the treatment of proliferative and differentiative disorders. Method (M2) is useful for diagnosing decreased fertility by examining FBPI in infertile individual. A pharmaceutical composition comprising a compound that modulates FBPI activity and a carrier is useful for the treatment of FBPI-related infertility. Method (M3) is useful for treating FBPI-related infertility, and method (M4) is useful for detecting an FBPI-related infertility disorder in a mammal, preferably humans. The compounds screened by method (M1) are useful for treating infertility, cancer, major opportunistic infections, immune disorders, and certain cardiovascular disorders. This sequence represents a human F-box protein.

SQ	Sequence 482 AA;					
Query Match	90.4%;	Score 2489;	DB 9;	Length 482;		
Best Local Similarity	98.1%;	Pred. No. 1.5e-215;				
Matches 472;	Conservative	5;	Mismatches 4;	Indels 0;	Gaps 0;	
QY	42	SNTRFTITLNYKDPITGDEETLASYGVSGDLICILQDDIPAPNIPSSSTDEHSSLQNN				101
Db	2	SNTRFTITLNYKDPITGDEETLASYGVSGDLICILHDDIPPPNIPSSSTDEHSSLQNN				61
QY	102	EQPSLATSSNQTSMQDEPSDSFQCAQAQSGVWDDSLGSPQNFEASIQDNAHMAEGT				161
Db	62	EQPSLATSSNQTSMQDEPSDSFQCAQAQSGVWDDSLGSPQNFEASIQDNAHMAEGT				121
QY	162	GFYPSEPMLCSESVGGVPHSLFTLYQSDACSDANDALIVLHLLMLESYIPQGTAKA				221
Db	122	GFYPSEPMLCSESVGGVPHSLFTLYQSDACSDANDALIVLHLLMLESYIPQGTAKA				181
QY	222	LSMPEKWLKSGVYKLYQYHPLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLP				281
Db	182	LSLPEKWLKSGVYKLYQYHPLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLP				241
QY	282	ESFICKEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTRAQALNLPDVGVLVPLELKL				341
Db	242	ESFICKEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTRAQALNLPVVGVLVPLELKL				301
QY	342	RIFRLDVRSLVLSAVCRDLFTASNDPLLRFLVLRDPRDNTVRVQDDTWKELYRKXHI				401
Db	302	RIFRLDVRSLVLSAVCRDLFTASNDPLLRFLVLRDPRDNTVRVQDDTWKELYRKXHI				361
QY	402	QRKESPKGRFVLLPSSTHTTIPFPNPLHPRFPSSRLPPGIIIGEYDQRTPLPVGDP				461
Db	362	QRKESPKGRFVLLPSSTHTTIPFPNPLHPRFPSSRLPPGIIIGEYDQRTPLPVGDP				421
QY	462	SSLIIPGGETPSQFPPLPRFPDVGPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSF				521
Db	422	SSLIIPGGETPSQFPPLPRFPDVGPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSF				481
QY	522	M 522				
Db	482	M 482				

RESULT 13  
AAU32109

ID	AAU32109	standard; protein; 607 AA.
XX	AC	AAU32109;
XX	DT	18-DEC-2001 (first entry)
XX	DE	Novel human secreted protein #2600.
XX	KW	Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX	OS	Homo sapiens.
XX	PN	WO200179449-A2.
XX	PD	25-OCT-2001.
XX	PF	16-APR-2001; 2001WO-US008656.
XX	PR	18-APR-2000; 2000US-00552929.
XX	PR	26-JAN-2001; 2001US-00770160.
XX	PA	(HYSE-) HYSEQ INC.
XX	PI	Tang YT, Liu C, Drmanac RT;
XX	DR	WPI; 2001-611725/70.
XX	PT	Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy.
XX	PS	Claim 20; Page 556; 765pp; English.
CC	CC	The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention
XX	SQ	Sequence 607 AA;
Query Match 88.9%; Score 2448.5; DB 4; Length 607; Best Local Similarity 90.8%; Pred. No. 9.6e-212; Matches 481; Conservative 7; Mismatches 33; Indels 9; Gaps 5;		
QY	1	MRLRVLLKRTWPLEVPETETLGHLSRLSLCTGWGSSNTRFTITLNYKDPITGDE 60
Db	36	MRLRVLLKRTWPLEVPETETLGHLSRLSLCTGWGSSNTRFTITLNYKDPITGDE 95
QY	61	ETLASYGVISGDLICILQDDIPAPNIPSTDSHSSLQNNQPSLATSSNQTSMQDEQP 120
Db	96	ETLASYGVISGDLICILQDDIPAPNIPSTDSHSSLQNNQPSLATSSNQTSMQDEQP 155
QY	121	SDSFQGAQAQSGVWDDSLGSPQNFEASIQDNAHMAEGTFYPSEPMLCSESVGGVQP 180
Db	156	SDSFQGAQAQSGVWDDSLGSPQNFEASIQDNAHMAEGTFYPSEPMLCSESVGGVQP 215
QY	181	HSLFTLYQSDACSDANDALIVLHLLMLESYIPQGTAKALSMPEKWLKSGVYKLYQYH 240
Db	216	HSLFTLYQSDACSDANDALIVLHLLMLESYIPQGTAKALSMPEKWLKSGVYKLYQYH 275

QY 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKEKLGENVANIYKD 300  
 DB 276 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKEKLGENVANIYKD 335  
 QY 301 LQKLSRLFKDQVLVPLLAFTQALNLPDVFGVLVPLLELKLRIFRLLDVRSVLSAVCR 360  
 DB 336 LQKLSRLFKDQVLVPLLAFTQALNLPDVFGVLVPLLELKLRIFRLLDVRSVLSAVCR 395  
 QY 361 DLFTASNDPLLWRFLYLRDFRNTVRYQDQTDWKELRYKRRHIQRKESPKGRFVMLLPSTH 420  
 DB 396 DLFTASNDPLLWRFLYLRDFRNTVRYQDQTDWKELRYKRRHIQRKESPKGRFVMLLPSTH 455  
 QY 421 TIFYPNPLHPRPPSSRLPPGIIGGEYDQRP-TLPYVYGDPISSILPGP-GETPS-QPFP 477  
 DB 456 TIFYPNPLHPRPPSSRLPPGIIGGEYDQRP-TLPYVYGDPISSILPGP-GETPS-QPFP 515  
 QY 478 -----LRPRFDPVGLPGNPILPGRGPNDRFPFRPSGRPTDGRLSFM 522  
 DB 516 TETHALNPSPPIISDRPNPQPCGAEAGPPNRRTPPPLRPOP-GGRANLM 564

## RESULT 14

ABB90109 ID ABB90109 standard; protein; 462 AA.

XX ABB90109;

XX 24-MAY-2002 (first entry)

XX Human polypeptide SEQ ID NO 2485.

XX Cytostatic; immunosuppressive; neurotropic; neuroprotective; antiviral;  
 KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; anti-ulcer;  
 KW vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic;  
 KW cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;  
 KW neurological disease; infection; human; secreted protein.

XX Homo sapiens.

XX WO200190304-A2.

XX 29-NOV-2001.

XX 18-MAY-2001; 2001WO-US016450.

XX 19-MAY-2000; 2000US-0205515P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Birse CE, Rosen CA;

XX WPI; 2002-122018/16.

XX N-PSDB; ABL90518.

XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and  
 PT prevention of neural, immune system, muscular, reproductive,  
 PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative  
 PT disorders.

XX Claim 11; SEQ ID NO 2485; 2081pp + Sequence Listing; English.

XX The invention relates to novel genes (ABL89449-ABL90853) and proteins  
 CC (ABB89040-ABB90444) useful for preventing, treating or ameliorating  
 CC medical conditions e.g. by protein or gene therapy. The genes are  
 CC isolated from a range of human tissues disclosed in the specification.  
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful in  
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and  
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,  
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune  
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic  
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,  
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)

CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing  
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)  
 CC infectious diseases such as viral, bacterial, fungal and parasitic  
 CC infections. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX

XX Sequence 462 AA;

Query Match 87.3%; Score 2404; DB 5; Length 462;  
 Best Local Similarity 88.1%; Pred. No. 6.6e-208;  
 Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

QY 1 MRLVRLIKRTPLEVPETETPLGLRSLRLSLCTWGYSSNTRFTITLNYKDLPTGDE 60

DB 1 MRLVRLIKRTPLEVPETETPLGLRSLRLSLCTWGYSSNTRFTITLNYKDLPTGDE 60

QY 61 ETLASYGIVSGDLICLIQDDIPAPNIPSSDSEHSSLQNNQPSLATSSNOTSQDDEP 120

DB 61 ETLASYGIVSGDLICLIQDDIPAPNIPSSDSEHSSLQNNQPSLATSSNOTSQDDEP 120

QY 121 SDSFGQAQSGVWDDSMGLPSONFEAESIQDNAHMAEGTGFYPSPEMCLSESVEGQVP 180

DB 121 SDSFGQAQSGVWDDSMGLPSONFEAESIQDNAHMAEGTGFYPSPEMCLSESVEGQVP 180

QY 181 HSLETLYQSADCSANDALIVLIHLLMLESYIPQGTAKALSMPKWKLSGVYKLYMH 240

DB 181 HSLETLYQSADCSANDALIVLIHLLMLESYIPQGTAKALSMPKWKLSGVYKLYMH 240

QY 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKEKLGENVANIYKD 300

DB 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKEKLGENVANIYKD 300

QY 301 LQKLSRLFKDQVLVPLLAFTQALNLPDVFGVLVPLLELKLRIFRLLDVRSVLSAVCR 360

DB 263 -----ALNLPDVFGVLVPLLELKLRIFRLLDVRSVLSAVCR 300

QY 361 DLFTASNDPLLWRFLYLRDFRNTVRYQDQTDWKELRYKRRHIQRKESPKGRFVMLLPSTH 420

DB 301 DLFTASNDPLLWRFLYLRDFRNTVRYQDQTDWKELRYKRRHIQRKESPKGRFVMLLPSTH 360

QY 421 TIFYPNPLHPRPPSSRLPPGIIGGEYDQRP-TLPYVYGDPISSILPGPGETPSQFPPLRP 480

DB 361 TIFYPNPLHPRPPSSRLPPGIIGGEYDQRP-TLPYVYGDPISSILPGPGETPSQFPPLRP 420

QY 481 RFDVVGPLPGNPILPGRGPNDRFPFRPSGRPTDGRLSFM 522

DB 421 RFDVVGPLPGNPILPGRGPNDRFPFRPSGRPTDGRLSFM 462

## RESULT 15

ADAS7586

ID ADAS7586 standard; protein; 462 AA.

XX ADAS7586;

XX 20-NOV-2003 (first entry)

XX Human secreted protein #566.

XX immunosuppressive; anti-inflammatory; antiasthmatic; antiallergic;  
 KW cytotatic; cerebroprotective; neuroprotective; neurotropic;  
 KW cardiovascular; antiarteriosclerotic; gene therapy;  
 KW human secreted protein; immune disorder; inflammation;  
 KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;  
 KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;  
 KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;  
 KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;  
 KW triple helix formation; antisense gene therapy; forensic biology.

XX Homo sapiens.

XX WO2002102994-A2.

XX 27-DEC-2002.

PD 19-MAR-2002; 2002WO-US008278.

PF 21-MAR-2001; 2001US-0277340P.

PR 19-JUL-2001; 2001US-0306171P.

PR 13-NOV-2001; 2001US-0331287P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA Rosen CA, Ruben SM;

XX WPI; 2003-167512/16.

FI N-PsDB; ADAS6693.

XX New human secreted polypeptides and polynucleotides, useful for

PT diagnosing, treating or preventing e.g. immune disorders, inflammatory

PT conditions, respiratory disorders, cancers, CNS disorders, or

PT neurodegenerative disorders.

XX Claim 13; SEQ ID NO 1779; 1754pp; English.

XX The invention relates to 592 new human secreted polypeptides useful for

CC diagnosing, treating or preventing e.g. immune disorders, inflammatory

CC conditions, respiratory disorders, cancers, CNS disorders, or

CC neurodegenerative disorders, or polypeptides comprising an amino acid

CC sequence at least 95% identical to the new sequences. The polypeptides,

CC antibodies or antibody fragments that bind to the polypeptides, nucleic

CC acids encoding the polypeptides, agonists or antagonists that binds to

CC the polypeptide, are useful in preparing diagnostic or pharmaceutical

CC compositions for diagnosing, treating or preventing an e.g. immune

CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,

CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and

CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders

CC (e.g. multiple sclerosis or ischemic brain injury), neurodegenerative

CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and

CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The

CC polynucleotides are useful for chromosome identification, chromosome

CC mapping, for controlling gene expression through triple helix formation

CC or antisense DNA or RNA, in gene therapy, for identifying individuals

CC from minute biological samples, in forensic biology, and as hybridization

CC probes. The polypeptides are useful for as molecular weight markers on

CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)

CC gels, to raise antibodies, for testing biological activities, and for

CC treating or preventing neural disorders, immune system disorders,

CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,

CC renal, proliferative and/or cancerous diseases. This sequence corresponds

CC to one of the polypeptide of the invention. Note: The sequence data for

CC this patent did form part of the printed specification, but was obtained

CC in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences.

XX SQ Sequence 462 AA;

Query Match 87.3%; Score 2404; DB 6; Length 462;

Best Local Similarity 88.1%; Pred. No. 6.6e-208;

Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

QY 1 MRLRVLRLKRTWPLEVPETPTLGHRLSHRLSLCTWGYSSNTRFTITLNYKDLPTGDE 60

DB 1 MRLRVLRLKRTWPLEVPETPTLGHRLSHRLSLCTWGYSSNTRFTITLNYKDLPTGDE 60

QY 61 ETLASYGVSGDLICLILODDIPAPNIPSSSTSEHSSIQNNEQPSLATSSNOTSMQDQOP 120

DB 61 ETLASYGVSGDLICLILODDIPAPNIPSSSTSEHSSIQNNEQPSLATSSNOTSXQDEOP 120

QY 121 SDSFOGQAQSGVWDDSMGLPSONFEASIQDNAHMAEGTGYFSEPMLCSESVEGVQP 180

DB 121 SDSFOGQAQSGVWDDSMGLPSONFEASIQDNAHMAEGTGYFSEPMLCSESVEGVQP 180

QY 181 HSLETLYQSADCSANDALIVLIHLLMLESYIPQGTAKALSMPEKWLKSGVYKLQYMH 240

Db 181 HSLETLYQSADCSANDALIVLIHLLMLESYIPQGTAKALSMPEKWLKSGVYKLQYMH 240

QY 241 PLCEGSSATLTCVPLGNLIVVNATLKKINNEIRS VKRLQLLPESFICKELGENVANIYKD 300

Db 241 PLCEGSSATLTCVPLGNLIVVN-----ALNLPDVFGLVVLPLELKLRIFFRLDVRSVLSAVCR 300

QY 301 LQKL SRLFKDQLVVYPLLAFTQALNLPDVFGLVVLPLELKLRIFFRLDVRSVLSAVCR 360

Db 263 -----ALNLPDVFGLVVLPLELKLRIFFRLDVRSVLSAVCR 300

QY 361 DLFTASNDPLLWRFLYLDRDPRDNTVRVQDPTDWKELYRKRHIQRKESPKGRFVMLLPSSSTH 420

Db 301 DLFTASNDPLLWRFLYLDRDPRDNTVRVQDPTDWKELYRKRHIQRKESPKGRFVMLLPSSSTH 360

QY 421 TIPFVYPNPLHPRPFSSRLPGIIGGEYDQRPPTLPYVGDPISSLIIPGGETPSQPPPLRP 480

Db 361 TIPFVYPNPLHPRPFSSRLPGIIGGEYDQRPPTLPYVGDPISSLIIPGGETPSQPPPLRP 420

QY 481 RFDVPVGPLPGNPILPQGGGNDPRFPFRPSRGRPTDGRLSFM 522

Db 421 RFDVPVGPLPGNPILPQGGGNDPRFPFRPSRGRPTDGRLSFM 462

Search completed: February 14, 2006, 20:57:47

Job time : 194 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 14, 2006, 20:58:08 ; Search time 41 Seconds  
(without alignments)  
1225.004 Million cell updates/sec

Title: US-09-927-458-2  
Perfect score: 2754  
Sequence: 1 MRLRVLLKRTWPLEVPETE.....DRFPFRSGRPTDGRLSFM 522  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	240.5	8.7	475	2	A86372
2	187.5	6.8	350	2	H86371
3	145.5	5.3	547	2	T46366
4	128.5	4.7	842	2	T32258
5	118	4.3	564	2	T70804
6	117.5	4.3	1213	2	A41724
7	117	4.2	403	2	S52796
8	116.5	4.2	915	2	T12526
9	116	4.2	4957	2	T03455
10	116	4.2	5262	2	T03454
11	112	4.1	1006	2	G86292
12	111.5	4.0	940	2	JE0291
13	111	4.0	1097	2	T49187
14	110.5	4.0	551	2	S57447
15	110	4.0	424	2	A54964
16	110	4.0	1468	2	S11515
17	109.5	4.0	742	2	A49672
18	109.5	4.0	772	2	A55004
19	109	4.0	741	2	I48694
20	109	4.0	1206	2	S24407
21	109	4.0	2783	1	A41948
22	108	3.9	311	2	T15997
23	108	3.9	577	2	T09024
24	107.5	3.9	589	2	T29299
25	107	3.9	351	1	JSBYP1
26	107	3.9	505	2	A53152
27	107	3.9	1257	2	T01020
28	106.5	3.9	212	2	S57330
29	106.5	3.9	584	2	G71676

30	106	3.8	401	2	T51407	proline-rich prote
31	106	3.8	444	2	E83802	hypothetical prote
32	105.5	3.8	828	2	T06133	hypothetical prote
33	105.5	3.8	882	2	T43250	spindle pole body-
34	105.5	3.8	897	2	A39405	beta-galactosidase
35	105.5	3.8	1465	2	T23056	chromodomain helic
36	105	3.8	502	2	A55197	Wiskott-Aldrich sy
37	105	3.8	715	2	G86239	protein P20824.6 (
38	104.5	3.8	235	2	A72594	hypothetical prote
39	104.5	3.8	301	2	J01663	hybrid proline-ric
40	104.5	3.8	850	2	JC5047	rae GTPase-activat
41	104	3.8	178	2	T36013	probable integral
42	104	3.8	188	2	D29149	proline-rich prote
43	104	3.8	574	2	H86467	probable transcrip
44	104	3.8	708	2	D96711	hypothetical prote
45	104	3.8	1252	2	D71810	probable type II D

ALIGNMENTS

RESULT 1

A86372

53.0K hypothetical protein F508.33 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C:Accession: A86372

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federapfel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Hughes, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: A86372

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-475 <STO>

A:Cross-references: UNIPROT:Q9ZUB8; UNIPARC:UPI000000ACSB6; GB:AE005172; NID:g4056460; P

C:Genetics:

A:Map position: 1

Query Match	8.7%	Score	240.5;	DB	2;	Length	475;
Best Local Similarity	24.5%;	Pred.	No. 9.1e-10;				
Matches	116;	Conservative	89;	Mismatches	177;	Indels	91;
Gaps	20;						
Qy	1	MRLRVLLKRTWPLEVPE	TEPTGLHLSRLSLCTGWYSSNTRFTITLNYKDPL--TG	58			
Db	3	LRURHHTRETLKLEADAD	-TLUHDURRINPTV-----PSSVHLSLNRKDELITPS	53			
Qy	59	DEETLASYGIVSGDLICLI	QDDIPAPNIPSSDSEHSSIQNNEQPSLATSSNQTQDE	118			
Db	54	PEDTLRSLGLISGLIVFSL	E-----ACESSNWKLRDSETVASQESNQTSHVD-	102			
Qy	119	QPSDSFGQQAQSGVQVND	SMGLQPSQNFEAESIQDNHMAEG--TGYPSPSPM-----	169			
Db	103	--SIGP-----AEVDVVP	DQAKSNPN-----TSVED-----PEGDISGMEGPEPMDVEQLDM	147			
Qy	170	--LCSESVESQVPHSL	ET--LYQADCSDDANDALIVLIHLLMLSEGYI--PQGT	218			
Db	148	ELAAAGSKRLSEPF	FLKNILLESKGTSELT--TLALSVAHVMLSEGFVLLNHGSKDNFS	206			
Qy	219	AKALSMPEKWLKSGVYK	QYMHPLCEGSSATLTCVPLGNLIVVNATL-----KINNI	271			
Db	207	KELLTVSLRYTLPELIK	SKDNTI---ESVSVKFQNLGPVVVVGTVGGSSGRVHMLDK	263			
Qy	272	-RSVKRLQLLPESFICKE	KLGENVANYKDQLKRLFKDQLVYPLLAFTRAQNLPLDVF	330			
Db	264	RRFPVPIDLVMDTST	SDSE---EGSSSYREVFMVKDRLVIPLLLIGICDKAGLEPPP	320			

QY 331 GLVVLPLELKLRIFFLLDVRSLVLSAVCRDLFTASNDPLLRFLYLRFRDNTVRV--Q 388  
Db 321 CLMLPTELKLELLELPGVSGNMACVCTEMRYLASNDLWKQCLSEVNFVVTAGD 380  
QY 389 DTDWK-----ELYRKRIHQRKESPKGRFVWMLLPSSHTTIPF 424  
Db 381 SVNWKARFATWRQKLAASDTPFRQNLGRNISTGRSGIRFRIIGDPPF 433  
RESULT 2  
H86371  
40.0K hypothetical protein F508.32 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: H86371  
R:Theologas, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Dewar, T.H.; Creasy, A.R.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.B.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: H86371  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-350 <STO>  
A:CROSS-references: UNIPROT:Q9ZUB9; UNIPARC:UPI00000A3C19; GB:AE005172; NID:g4056459; PI  
C:Genetics:  
A:Map position: 1  
Query Match 6.8%; Score 187.5; DB 2; Length 350;  
Best Local Similarity 24.4%; Pred. No. 4.2e-06;  
Matches 90; Conservative 58; Mismatches 118; Indels 103; Gaps 17;  
QY 172 SESVEGVQVPHLE-----TLYOSADCSNDALIVLHLLMLESYI 213  
Db 22 NSGIEGVPMDVLAALAAKSKRLSEPFLLKNVLLKSGDTSOLT-ALALSVAHVMLESGV 80  
QY 214 --PGTE-----AKALSMPEKWLKSGVYKLYMHPLCEGSSATLTCVPLGNLIVNATL- 265  
Db 81 LLDHGSDFKFSKLLSLVSLRYTLPELITRKDNTV---ESVTVRFQIGRPLVVGTLG 137  
QY 266 ---KINNEIRSVKRLQLLPESFICEKEL---GENVANYIKDQKLSRLFKDQVYPLIA 318  
Db 138 GSCKEVH--WTSLSKSRFLPVIDLVDTLKPEKQSSSYREVFMWVMDLVIPLL- 194  
QY 319 FTRQALNLPDVG-----LVVLPLELKLRIFFLLDVRSLVLSAVCRDLFTASNDPLLM 372  
Db 195 -----IGLCDRAGLSPCLMLPTELKLELLELPGVSGNMACVCTEMRYLASNDLW 249  
QY 373 RFLYLRDFRDNTVRVQ--DWDKELY-----RKR--HQRKESPKGRFVWMLLPSSHTTIP 423  
Db 250 EHKCLEGKGLWKLKLYGTGDVMDKRXKSFASFRWRKRLDLLARRNPPIKK----- 296  
QY 424 FVPNPLHRPPSSRLPPGLIGGEDQRPRTLPPYVGDPISSLIPGPGETPSQPPL----- 478  
Db 297 --SNRPFLLPDDR-----DRREPDRFG-----PSDFYRFLGRDP 331  
QY 479 RPRDPVGP 487  
Db 332 RDRFGFRDP 340  
RESULT 3  
T46366  
hypothetical protein DKFZp434C0118.1 - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 09-Jul-2004

C:Accession: T46366

R:Ottewaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, January 2000

A:Reference number: Z23031

A:Accession: T46366

A&gt;Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-547 &lt;AAA&gt;

A:CROSS-references: UNIPROT:Q9NT57; UNIPARC:UPI000007107F; EMBL:AL1137520

A:Experimental source: adult testis; clone DKFZp434C0118

C:Genetics:

A:Note: DKFZp434C0118.1

Query Match 5.3%; Score 145.5; DB 2; Length 547;

Best Local Similarity 21.7%; Pred. No. 0.0094;

Matches 98; Conservative 61; Mismatches 123; Indels 169; Gaps 24;

QY 105 SLATSSNQTSQMDQPSDSFQQAQSGVWDDSMLG-PSQNFEAESIQDNAHMAEGTGF 163

Db 72 SAAETGSRHPDTHPSS--GGRCRGTSPSSAAGRPAASMAEAE---EDCH----- 119

QY 164 YPSEPMLCSEVGEQVPHSLETLVQSADCSNDALIVLHLLMLESYIIFQGTAKA-L 222

Db 120 -----SDTVR-----ADDDSENES-----PAETDLQAL 143

QY 223 SMPEKWLKSGVYKLYMHPLCEG-SSATLTCVPL---GNLIVNATLKNNE----- 270

Db 144 QM-----FRAQWMPFELAPGVSSNLENRRCRAARGLQKTSADTKGQEQKESKA 194

QY 271 ----IRSV-----KRLQLLPE-----SFICKEKLGENVANIY---KDLQ 302

Db 195 RELFLKAVEEQNGALYEAIFYRRAMQLVDPDIEFKITYTTRSPDGDGVNSYIEDNDDDS 254

QY 303 KLSRL----FKDQLVYPLLAFTROALNL--PDV-----FGLVVLPLELKLRIFFL- 348

Db 255 KWADLLSYFOQ-----LTFQESVLKLCQPELESSQIHISVLPMEVLMIYIFRWVVSDDL 309

QY 349 VRSVLISAVCRDLFTASNDPLLRFLYLRFRDNTVR-VODTDWKELYRKRHIQRKESP 407

Db 310 LRSLEQLSLVCKGFIICARDPEIWRACLKLVGWSCKIKLVYTTSWRENFLER-----P 362

QY 408 KGRFVMLLPSS-----HTIPYFNPPLHPRFPFSSRLPGLIIGGEYDQ 450

Db 363 RVREDGVVISKTTVIRQGEQSLDGFYRAWHQVEYI---RYIRFFPDGHV----- 408

QY 451 RPTLPYVGDPDIPSSILPGGETPSQFPPLRPR 481

Db 409 -----MMLTTPPEPQSIVPLRLTR 427

## RESULT 4

T32258

hypothetical protein C24A1.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004

C:Accession: T32258

R:Connell, M.

submitted to the EMBL Data Library, September 1997

A:Description: The sequence of C. elegans cosmid C24A1.

A:Reference number: Z21141

A:Accession: T32258

A&gt;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-842 &lt;CON&gt;

A:CROSS-references: UNIPROT:O17055; UNIPARC:UPI000017B7AE; EMBL:AF024491; PIDN:AAB70312

A:Experimental source: strain Bristol N2; clone C24A1

C:Genetics:

A:Gene: CESP:C24A1.3

A:Map position: 3

A:introns: 43/2; 189/3; 234/1; 351/1; 511/3; 578/3; 594/2; 636/2; 675/3

Query Match 4.7%; Score 128.5; DB 2; Length 842;

Best Local Similarity 20.3%; Pred. No. 0.31;





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Qy 467 -----GGETSQF---PPLRRF-----DPVGLPGNPILPGEGGNDRFPFRPSRGR 513
Db 685 PPLTGPSTVTHFAFGPPLPQLSEGCGRDFOAPAPPAPPLPGLGPPVP--PPLPGSGL 742
Qy 514 P 514
Db 743 P 743

RESULT 7
S52796
prpL2 protein - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-May-1995 #sequence_revision 10-Nov-1995 #text_change 10-Sep-1997
C:Accession: S52796
R:Ruhlmann, A.; Kreideweiss, S.; Nordheim, A.
submitted to the EMBL Data Library, March 1995
A:Reference number: S52796
A:Accession: S52796
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-403 <RUH>
A:Cross-references: UNIPARC:UPI000017C32C; EMBL:X86019; NID:g762951

Query Match 4.2%; Score 117; DB 2; Length 403;
Best Local Similarity 32.9%; Pred. No. 0.72;
Matches 46; Conservative 9; Mismatches 41; Indels 44; Gaps 9;

Qy 415 LPSSTHTTPFVNPILHPPFPSSR-----LPGIIGGVYDORPTLPYVGDPTISSL---IP 466
Db 203 VPSTPR--PSAPHRHLAPPPSRGPPPLPPSSGN--DETPLPQRLNLSSTTPPLP 258
Qy 467 GPGET-----PSQFPPLRFRDP--VGPLPGNPFI-----LPG----- 497
Db 259 SPGRSGPLPPVPVSRPPPPVDRDPRGSGPLPPPPVSVRNGSTSRALPATQLPGRSGVD 318
Qy 498 --RGGPNDRF--PFRPSRGRP 514
Db 319 SPRSGPRPPLPPDRPSAGAP 338

RESULT 8
T12526
hypothetical protein DKFp434M183.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C:Accession: T12526
R:Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A:Reference number: Z17524
A:Accession: T12526
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-915 <WAM>
A:Cross-references: UNIPROT:Q9Y4Q8; UNIPARC:UPI0000070795; EMBL:AL080141
A:Experimental source: adult testis; clone DKFp434M183
C:Genetics:
A:Note: DKFp434M183.1

Query Match 4.2%; Score 116.5; DB 2; Length 915;
Best Local Similarity 20.7%; Pred. No. 2.6;
Matches 129; Conservative 76; Mismatches 208; Indels 209; Gaps 36;

Qy 34 LLCTWGYSSNTRFTITLNY-KDPLTGDDETLASYGIVSGDLICLILQDDIPAPNIPSTSD 92
Db 205 LKVTLEQDSRMKFLKLGYSKDEL---QKKVATW-----LKSVDV---GLGESFQ 247
Qy 93 SEHSSLQNEQPSLATSNTQMSQDEQPSDSFGQAQSGV--W-----NDDSM----- 139
Db 248 PKGNDLNSDRQAFCQSQASKHTKEASASAFFDELVPQNMTPWEIPITKIDIGLLSQAL 307
Qy 140 ----LGPSON--FEAESIQDNAHMAEGTGF----YPSFPMLCSESVQGVPHSLTTLQSS 189
```

```
Db 308 LLGELGPAVELCLKEERFADAILAQAGGTDLLAKQTQERYLAKKKT--KISSLLACVVQK 365
Qy 190 -----ADCSAN--DALIVLIHLLMLESYIPOGTAKALSMPEKWKLSGVYKLYQWHP 241
Db 366 NWKDVVCTCSLKWNREALALITY-----SGTE-----KFPDELCDMLTRMEQ----- 408
Qy 242 LCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICK--EKLGENVANIY 298
Db 409 --EGSRA-----LTSEARL-----CYVCSGSVERLVECAKCH 439
Qy 299 KDLQKLSRLFKDQLVYPLLAFTROALNLPDVFGLVVLPLELKLRIFRLLDVRSLV----- 353
Db 440 --QALSPMALQDLMEKVMVNLRSLEQLRGPHGVSPGP-----ATTYRVQYANLLAAQGS 492
Qy 354 ---SLSAVCRD-----LFTASNDPLLNR-----FLYLRDFRDNTRVQDTHKE 394
Db 493 LATAMSPFLPRDCAOPVQQLRDLFHAQGSVALQQSPPPFPFPRIVVGVTILHSETSSYR 552
Qy 395 L-YRKRIHQKESPKGRFVMLLPSSHTTIPYPNPLHPRPPSSR----- 438
Db 553 LGSQPSHQVPTPSRPR--VFTPOSSPAMPLAPS--HPSPYQGPRTONISYRAGPQAI 608
Qy 439 ---LPPGI-----IGGEYDQRP-----TLPVVGDPFISSLIPG---PG-----E 470
Db 609 QPLPLSFQVRPASSQPQLLGGQRYOVNPNVGFPGTWPPLPGSPLPWACPGIMRPGSTSLPE 668
Qy 471 TPSQFP--PLRP-----RDPVGPLPGNPILPG-----RGGND 503
Db 669 TPLRFLPLPLRPLGFGRMVSHTPAPPASFVPVYLPDGPAPCASSVLPTTGILTPHGPQD 728
Qy 504 RPFPRPS-RGRPTDGL--SPM 522
Db 729 SWKEAPAPRGNLQRNKLPTETFM 750

RESULT 9
T03455
ALR protein - human
C:Species: Homo sapiens (man)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C:Accession: T03455
R:Prasad, R.; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R.; Yano,
Oncogene 15, 549-560, 1997
A:Title: Structure and expression pattern of human ALR, a novel gene with strong homolog
A:Reference number: Z14954; MUID:97388474; PMID:9247308
A:Accession: T03455
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-4957 <PRA>
A:Cross-references: UNIPROT:O14686; UNIPARC:UPI00001100F1; EMBL:AF010404; NID:g2358286;
C:Genetics:
A:Gene: ALR
A:Map position: 12
A:Superfamily: acute lymphoblastic leukemia protein, ALR type
C:Keywords: alternative splicing

Query Match 4.2%; Score 116; DB 2; Length 4957;
Best Local Similarity 20.0%; Pred. No. 35;
Matches 102; Conservative 64; Mismatches 181; Indels 164; Gaps 25;

Qy 94 EHSSLQNEQPSLATSNTQMSQDEQPSDSFGQAQSGV--GVMNDD-SMLGPSQNFSAES 150
Db 3356 QQQQLQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 3409
Qy 151 IQDNAHMAEGTGFVPSEPM-----LCSESV----- 176
Db 3410 -QQQQQVALGFGM-PAKPLQHFSSPGALGPTLLLTGKEQNTVDPAVSSEATEGPTHQGG 3467
Qy 177 ---GQVPHSLTLYQSADCSANDALIVLIHLLMLESYIPQ-GTEAKALSMPEKWKLS 231
Db 3468 PLAIGTTPESMATEPGEVKPSLSGDSQLLVQ-----PQPOPSSQLQLOPPLRLP 3518
```



Qy 232 GYVKLQ--YMH-----PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLP 281  
Db 3519 GQQQQVSLHTAGGGSHGLGSSSEASSVP---HLLAQPSVSLGDPQGSMTQNLGPR 3575  
Qy 282 ESFICKEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTTRQALNLPDVFLVVLPLELKL 341  
Db 3576 QQPMLERPQNNTGP-----QPPKPGFVL---QSGQGLP---GVGIMPTVGQL 3617  
Qy 342 RIFRLLDVRSVLSLAVCRDLFTASNDPLLRFLYLRDRFNTVRVQDTPWKELYRKRI 401  
Db 3618 R-----AQLOGLVAKNPQLRHLSPOQQQL-----QALLMQRL 3651  
Qy 402 QKESPKGRFVMLLP-----SSTHTIPF-----YNNP-----LHRRPPPS 436  
Db 3652 QQSOA-----VRQTPPYQEPCTQTSPLQGLGCPQLGFGFPGQTGPLQELGAGPRPOGP 3706  
Qy 437 SRL--PPGIIGGEYDQRTPLPYVG-----DPISSLIPGPGTSPQFPPLRPRDFVCGPLP 489  
Db 3707 PRLPAPPGALS-----TGPVLGVHPTPPSS--POEPRKPSQLPSPSSQLPTEAQLP 3757  
Qy 490 GPNPILPGRGPNDRFPFRPSRGRPTDGRLS 520  
Db 3758 PTHGTPKPGQFTLEPP--PGRVSPAAQA 3786

RESULT 10  
T03454  
ALR protein - human  
C:Species: Homo sapiens (man)  
C:Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 09-Jul-2004  
C:Accession: T03454  
R:Prasad, R.; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Druck, T.; Rallapalli, R.; Yano, Oncogene 15, 549-560, 1997  
A:Title: Structure and expression pattern of human ALR, a novel gene with strong homolog A:Reference number: Z14954; MUID:97388474; PMID:9247308  
A:Accession: T03454  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-5262 <PRA>  
A:Cross-references: UNIPROT:O14686; UNIPARC:UPI0000110107; EMBL:AF010403; NID:G2358284;  
C:Genetics:  
A:Gene: ALR  
A:Map position: 12  
C:Superfamily: acute lymphoblastic leukemia protein, ALR type  
C:Keywords: alternative splicing

Query Match 4.28; Score 116; DB 2; Length 5262;  
Best Local Similarity 20.08; Pred. No. 38;  
Matches 102; Conservative 64; Mismatches 181; Indels 164; Gaps 25;

Qy 94 EHSSLQNEQPSLATSSNQTSMDQPSDFQGAQAS--GVWNDD-SMLGPSQNPFAES 150  
Db 3661 QQQQLQQQQQQQLQQQQQQQLQQQQQQQQQQQQQQQQQQQQQLNQSLTLLSPQQ----- 3714  
Qy 151 IQNAHMAETGTFVPSBP-----LCSSEV----- 176  
Db 3715 -QQQQQVALGFGM-PAKPLQHFSPGALGPTLLLTGKEQNTVDPVAVSSEATEGPTSHQGG 3772  
Qy 177 ----GQVPHSELTLYQSADCSANDALIVLHLLMLESVIQO-GTEAKALSMPKWKLS 231  
Db 3773 PLAIGTTPESMATEPGEVKPSLSDGSLQLLVQ-----POQPQPSQLQPLRLP 3823  
Qy 232 GYVKLQ--YMH-----PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLP 281  
Db 3824 GQQQQVSLHTAGGGSHGLGSSSEASSVP---HLLAQPSVSLGDPQGSMTQNLGPR 3880  
Qy 282 ESFICKEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTTRQALNLPDVFLVVLPLELKL 341  
Db 3881 QQPMLERPQNNTGP-----QPPKPGFVL---QSGQGLP---GVGIMPTVGQL 3922  
Qy 342 RIFRLLDVRSVLSLAVCRDLFTASNDPLLRFLYLRDRFNTVRVQDTPWKELYRKRI 401  
Db 3923 R-----AQLOGLVAKNPQLRHLSPOQQQL-----QALLMQRL 3956

Qy 402 QKESPKGRFVMLLP-----SSTHTIPF-----YNNP-----LHRRPPPS 436  
Db 3957 QQSOA-----VRQTPPYQEPCTQTSPLQGLGCPQLGFGFPGQTGPLQELGAGPRPOGP 4011  
Qy 437 SRL--PPGIIGGEYDQRTPLPYVG-----DPISSLIPGPGTSPQFPPLRPRDFVCGPLP 489  
Db 4012 PRLPAPPGALS-----TGPVLGVHPTPPSS--POEPRKPSQLPSPSSQLPTEAQLP 4062  
Qy 490 GPNPILPGRGPNDRFPFRPSRGRPTDGRLS 520  
Db 4063 PTHGTPKPGQFTLEPP--PGRVSPAAQA 4091

RESULT 11  
G86292  
hypotheical protein F7H2.17 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: G86292  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federapfel, N.A.; Kaul, S.; White, O.; Alonso, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: G86292  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1006 <STO>  
A:Cross-references: UNIPROT:Q9LMQ1; UNIPARC:UPI00000A3407; GB:AE005172; NID:g8927662;  
C:Genetics:  
A:Map position: 1

Query Match 4.18; Score 112; DB 2; Length 1006;  
Best Local Similarity 32.78; Pred. No. 6.4;  
Matches 36; Conservative 6; Mismatches 48; Indels 20; Gaps 3;

Qy 406 SPKGRFVMLLPSSTHTIPFYNPPLHPRPFPSSRLPPGIIIGGEYDQRTPLPVGDPISSLI 465  
Db 88 SPENPLFPQP-----PRPPRRPRPRPSRLPP-----PLVPSPPPLH 128  
Qy 466 PPGETPSQFPPLRPRDFVCGPLPGPNPILPGRGPN-DRFPFRPSRGRP 514  
Db 129 PRSPCPPLPSPPLVPSPPPPPSPLVPSPPPPPSPPPPPPPPPPPPPPPP 178

RESULT 12  
JE0291  
FB19 protein - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 09-Jul-2004  
C:Accession: JE0291  
R:Rotaro, A.; Grifa, A.; Carella, M.; Rommens, J.M.; Valentino, M.A.; Roetto, A.; Zelan Biochem. Biophys. Res. Commun. 250, 555-557, 1998  
A:Title: Cloning of a new gene (FB19) within HLA class I region.  
A:Reference number: JE0291; MUID:99003493; PMID:9784381  
A:Accession: JE0291  
A:Molecule type: mRNA  
A:Residues: 1-940 <TOT>  
A:Cross-references: UNIPROT:O00405; UNIPARC:UPI0000072B3F; GB:Y13247; NID:g2117158; PID  
C:Genetics:  
A:Gene: FB19  
A:Map position: 6p21.3

Query Match 4.08; Score 111.5; DB 2; Length 940;  
Best Local Similarity 36.88; Pred. No. 6.3;  
Matches 39; Conservative 6; Mismatches 40; Indels 21; Gaps 6;

Qy 424 FYPNPLHPPSPSRLPGLIGGEVDQRTLPYVGDPISSILPGGETSPQFPPLRPFD 483  
Db 643 FPPGPGGMPGPHGG-FCGPVGPRLLPPLPPRGGDPFWD---GPGD-PMRGGPMRG--- 694  
Qy 484 PVGLPGFNPLPGRGG-----PNDRPFPPPSR-----GRPTDGR 518  
Db 695 --GPGPGPYHRRGGRGNGNEPPPPPPFRGARGSGSGGPPNCR 738  
RESULT 13  
T49187  
hypothetical protein MAA21.90 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 09-Jul-2004  
C:Accession: T49187  
R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, K.  
submitted to the Protein Sequence Database, April 2000  
A:Reference number: 225018  
A:Accession: T49187  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1097 <RIE>  
A:Cross-references: UNIPROT:Q9LY69; UNIPARC:UPI00000A03E7; EMBL:AL1163818; GSPDB:GNO0061;  
A:Experimental source: cultivar Columbia; BAC clone MAA21  
C:Genetics:  
A:Gene: ATSP:MAA21.90  
A:Map position: 3  
A:Introns: 106/2; 124/3; 165/3; 198/1; 210/2; 245/3; 265/1; 297/3; 337/3; 352/1; 394/1;  
Query Match 4.0%; Score 111; DB 2; Length 1097;  
Best Local Similarity 20.2%; Pred. No. 8.7; Mismatches 218; Indels 146; Gaps 26;  
Matches 111; Conservative 75; Mismatches 218; Indels 146; Gaps 26;  
Qy 37 TWGY-----SSNRTFTITLYKDKPLTGDTEETLASGVISGDLICLIQDD-IPAPN 86  
Db 435 TWGLLKIMFEEGSTRKLSHLGFTLPVAEKQAVDG---LSSDLNGIRLEDTAADALD 491  
Qy 87 IPSSTDSHSLQNEQ-----PSLATSNQTSMDQSPD---SFQGAQAQSGVWNDD 138  
Db 492 LDDSENAFAFMDNGEDFNNFPAPKDPVSTSAKDFMPSDTDFSTKGEETQEMOESEE 551  
Qy 139 MLGP-----SQNFAESIQDN---AHMAEGTGFPYS--EPMLCSES 174  
Db 552 SSDPVDNAIORALIVGYKRAVDCCITANKMADALVIAHG-GTALWESTREKYLKTS 610  
Qy 175 -----VEGVPHSLTLYQADCSNDANDALITVLHLLMLESXYIPOQTEAKALSMPEKW 228  
Db 611 APYMKVSAWVNDLRSLLIYTRSHKFWKETLALLC-----TFAQGEQW 653  
Qy 229 KLSGVYKLQYWHPLCEGSSATLTCVPLGN-LIVVNATLKINNEIRSVKRLQLLPESFICK 287  
Db 654 T-----TLCDALASKL--MAAGNTLAALVLCYCAGNVDRIVE-----IWSRSLAN 696  
Qy 288 EKLGENVANIYKOLKLSRLFKDQVLYPLA-----FTRQALNLPDVGVLVLP---LELK 340  
Db 697 ERDRGSYAEILLQDLMEKT-----LVLATGNTKKFSASLCKLFESYAEILASQGLLTTA 750  
Qy 341 LRIFRLLD-----VRSVLSISAVCRDLFTAS-----NDPLLMLRFLYL 378  
Db 751 MKYLVLDGGGLSPSLTILDRISABETNTTASGNTQPOSTWYVQEPFQAQPNVLA 810  
Qy 379 DFRONTVRVDQTDWKELYRKRIORKEGPKGRFVMLPSSHTTIP---FYPNPLHPPFP 435  
Db 811 NPYDNQYQPYTDSYVYVQVSH-----PPMQQPTFMFPHQAQAPQPSFTAPT--SNAQP 864  
Qy 436 SSR-----LPGLIGGEVDQRTLPYVGDPISSILPGGETSPQFPPLRPFDVGL- 488  
Db 865 SMRTTFVSTPALKNADQYQQFTWS-----SHSFTGFSNNAYVPVPPGQYAPSGPSQ 918  
Qy 489 --PGNPILP 496  
Db 919 LGQYFNPKM 928

RESULT 14

S57447  
HPBRII-7 protein - human  
N:Alternate names: HPBRII-4 protein  
C:Species: Homo sapiens (man)  
C:Date: 10-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 05-Oct-2004  
C:Accession: S57447; S57489  
R:Fleischhauer, K.L.  
submitted to the EMBL Data Library, June 1992  
A:Reference number: S57447  
A:Accession: S57447  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-551 <FILE>  
A:Cross-references: UNIPROT:Q16630; UNIPARC:UPI000006D566; EMBL:X67336; NID:9871300; PID:  
A:Accession: S57489  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-551 <FL2>  
A:Cross-references: UNIPARC:UPI000006D566; EMBL:X67337; NID:9871298; PID:CAA47752.1; PI:  
C:Genetics:  
A:Introns: 231/3  
F:82-151/Domain: ribonucleoprotein repeat homology <RRM4>  
Query Match 4.0%; Score 110.5; DB 2; Length 551;  
Best Local Similarity 31.1%; Pred. No. 3.4;  
Matches 41; Conservative 9; Mismatches 39; Indels 43; Gaps 8;  
Qy 408 KGRFVMLLPSSHTTHIPFVNPL----HPRPPPSRLPGLIGGEVDQRTLPYVGDPISS 463  
Db 204 RGRPPGAVGGDR----FPGPAGGPPPPPPACQTTP-----RPLGPGGPPGPP 250  
Qy 464 LIPEGGET---PSQFPPLR-----PRFDPVGLP-PGPNPILPGRGPN 502  
Db 251 GPPPPGGVLPPLAGPPNRRGDRPPPPVLPFGQPFQGP---PLGLPLPPGPPPPVPGYGPP 307  
Qy 503 DRFFPFRSRRP 514  
Db 308 G--PPPPQQGPP 317  
RESULT 15  
A54984  
spliceosome-associated protein SAP-49 - human  
C:Species: Homo sapiens (man)  
C:Date: 23-Mar-1995 #sequence\_revision 05-Apr-1995 #text\_change 31-Dec-2004  
C:Accession: A54984  
R:Champion-Arnaud, P.; Reed, R.  
Genes Dev. 8, 1974-1993, 1994  
A:Title: The prespliceosome components SAP 49 and SAP 145 interact in a complex implicat  
A:Reference number: A54964; MUID:95047348; PMID:7959871  
A:Accession: A54964  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-424 <CHA>  
A:Cross-references: UNIPROT:Q15427; UNIPARC:UPI0000135472; GB:L35013; NID:g556216; PID:  
F:14-81/Domain: ribonucleoprotein repeat homology <RRM4>  
F:101-169/Domain: ribonucleoprotein repeat homology <RRM2>  
Query Match 4.0%; Score 110; DB 2; Length 424;  
Best Local Similarity 32.0%; Pred. No. 2.5;  
Matches 39; Conservative 9; Mismatches 32; Indels 42; Gaps 9;  
Qy 430 HPRPPPSRLP-PGI-----IG-----GEYDQRTLPYVGDPISSILPGPG 469  
Db 292 HPHPFPFGMHPHGMQSLAHGPHGLGHAGPGSGGQPPPPPPPG-----MPHPG 345  
Qy 470 ETPSQFPLPRP-DPV---GFLP-----GNPILPGRG--GPNDRFPFRSRG-----R 513  
Db 346 PPMGMGPRGPPFGSPMGHPGMPMPHGMGRGPPPLMPHPHGTGTPRPPPYGYQRGLPPPR 405

Qy 514 PT 515  
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Db 406 PT 407

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Job time : 46 secs

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OM protein - protein search, using sw model

Run on: February 14, 2006, 21:13:14 ; Search time 168 Seconds  
(without alignments)  
1298.255 Million cell updates/sec

Title: US-09-927-458-2  
Perfect score: 2754  
Sequence: 1 MLRLVRLKRTWPLEVPETE.....DRPFPRSGRPTDGRLSFM 522

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2754	100.0	522	3	US-09-927-458-2
2	2754	100.0	522	4	US-10-245-593-2
3	2744	99.6	522	4	US-10-679-246-10
4	2489	90.4	482	4	US-10-042-417-14
5	2489	90.4	482	5	US-10-652-928-14
6	2489	90.4	482	6	US-11-073-485-14
7	2489	90.4	482	6	US-11-073-470-14
8	2404	87.3	462	3	US-09-397-945-200
9	2404	87.3	462	4	US-10-264-237-2485
10	2404	87.3	462	4	US-10-653-595-200
11	2404	87.3	497	3	US-09-397-945-435
12	2404	87.3	497	4	US-10-653-595-435
13	2270	82.4	443	4	US-10-679-246-8
14	2086.5	75.8	549	5	US-10-450-763-48869
15	1527	55.4	317	4	US-10-264-237-2484
16	1238	45.0	231	4	US-10-408-765A-752
17	1086	39.4	221	4	US-10-094-749-1723
18	714	25.9	174	3	US-09-397-945-434
19	714	25.9	174	4	US-10-653-595-209
20	714	25.9	174	4	US-10-653-595-434
21	714	25.9	175	3	US-09-397-945-209
22	396	14.4	76	4	US-10-029-386-27908
23	299	10.9	113	5	US-10-820-474A-133
24	265.5	9.6	225	5	US-10-450-763-37197
25	264.5	9.6	53	5	US-10-450-763-48868
26	249	9.0	47	4	US-10-029-386-33496
27	215.5	7.8	500	5	US-10-739-930-9910

28	211	7.7	485	4	US-10-425-114-59910	Sequence 59910, A
29	207	7.5	485	4	US-10-425-114-59131	Sequence 59131, A
30	201	7.3	485	4	US-10-425-114-60984	Sequence 60984, A
31	198	7.2	447	4	US-10-425-115-349540	Sequence 349540,
32	194	7.0	39	4	US-10-042-417-21	Sequence 21, Appl
33	194	7.0	39	5	US-10-652-928-21	Sequence 21, Appl
34	194	7.0	39	6	US-11-073-485-21	Sequence 21, Appl
35	194	7.0	39	6	US-11-073-470-21	Sequence 21, Appl
36	189	6.9	38	3	US-09-801-348-47	Sequence 47, Appl
37	164	6.0	38	3	US-09-801-348-49	Sequence 49, Appl
38	147	5.3	270	6	US-11-097-143-19197	Sequence 19197, A
39	144	5.2	408	4	US-10-284-237-1835	Sequence 1835, Ap
40	142	5.2	1131	4	US-10-425-115-355048	Sequence 355048,
41	140	5.1	379	4	US-10-264-049-2807	Sequence 2807, Ap
42	139	5.0	327	4	US-10-042-417-58	Sequence 58, Appl
43	139	5.0	327	4	US-10-679-246-12	Sequence 12, Appl
44	139	5.0	327	5	US-10-652-928-58	Sequence 58, Appl
45	139	5.0	327	6	US-11-073-485-58	Sequence 58, Appl

ALIGNMENTS

RESULT 1  
US-09-927-458-2  
; Sequence 2, Application US/09927458  
; Patent No. US20020058024A1  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, David  
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNG/NGF RECEPTOR  
; TITLE OF INVENTION: AND OTHER PROTEINS  
; FILE REFERENCE: WALLACH=22A  
; CURRENT APPLICATION NUMBER: US/09/927,458  
; CURRENT FILING DATE: 2001-08-13  
; PRIOR APPLICATION NUMBER: PCT/IL98/00125  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: IL 120485  
; PRIOR FILING DATE: 1997-03-19  
; PRIOR APPLICATION NUMBER: 09/381,358  
; PRIOR FILING DATE: 1999-09-20  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 522  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-927-458-2

Query Match 100.0%; Score 2754; DB 3; Length 522;  
Best Local Similarity 100.0%; Pred. No 2.6e-223;  
Matches 522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MLRLVRLKRTWPLEVPETEPTLGLHLSHLRLSLCTGWYSSNTRFTITLNYKDLPTGDE	60
Db	1	MLRLVRLKRTWPLEVPETEPTLGLHLSHLRLSLCTGWYSSNTRFTITLNYKDLPTGDE	60
Qy	61	ETLASYGIVSGDLICILQDDIPAPNIPSTDSHSLQNEQPSLATSSNQTSMQDEQP	120
Db	61	ETLASYGIVSGDLICILQDDIPAPNIPSTDSHSLQNEQPSLATSSNQTSMQDEQP	120
Qy	121	SDSFQGAAGQGVNDDMLGPSONFAESIQDNNAHMAEGTGFYPSPEMLCSBSVEGQVP	180
Db	121	SDSFQGAAGQGVNDDMLGPSONFAESIQDNNAHMAEGTGFYPSPEMLCSBSVEGQVP	180
Qy	181	HSLETLQSQADCSANDALIVLHLLMESGYIPQGTAKALSMPEKWLKSGVYKQYMH	240
Db	181	HSLETLQSQADCSANDALIVLHLLMESGYIPQGTAKALSMPEKWLKSGVYKQYMH	240
Qy	241	PLCEGSSATLTCVPLGNLIVVNATLKNNEIRSVKRLQLLPESICKEKLGENVANIYKD	300
Db	241	PLCEGSSATLTCVPLGNLIVVNATLKNNEIRSVKRLQLLPESICKEKLGENVANIYKD	300

Qy 301 LQKLSRLFKDQLVYPLLAFTRAQALNLPDVFGVLVPLLELKLRIFFLLDVRSLSAVCR 360  
Db 301 LQKLSRLFKDQLVYPLLAFTRAQALNLPDVFGVLVPLLELKLRIFFLLDVRSLSAVCR 360  
Qy 361 DLFTASNDPLLRFLYLDRFDNTVRVQDQDPTLPGVGDPISSLLPGGETPSQPPPLRP 420  
Db 361 DLFTASNDPLLRFLYLDRFDNTVRVQDQDPTLPGVGDPISSLLPGGETPSQPPPLRP 420  
Qy 421 TIPFVNPPLHPRPPSSRLPGIIGGEYDQDPTLPGVGDPISSLLPGGETPSQPPPLRP 480  
Db 421 TIPFVNPPLHPRPPSSRLPGIIGGEYDQDPTLPGVGDPISSLLPGGETPSQPPPLRP 480  
Qy 481 RFDVGPPLPGNPILPGRGGNDPRFPFRPSRGRPTDGRLSFM 522  
Db 481 RFDVGPPLPGNPILPGRGGNDPRFPFRPSRGRPTDGRLSFM 522  
Qy 481 RFDVGPPLPGNPILPGRGGNDPRFPFRPSRGRPTDGRLSFM 522  
Db 481 RFDVGPPLPGNPILPGRGGNDPRFPFRPSRGRPTDGRLSFM 522  
RESULT 2  
US-10-245-593-2  
; Sequence 2, Application US/10245593  
; Publication No. US20030039646A1  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, David  
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNG/NGF RECEPTOR H  
; FILE OF INVENTION: AND OTHER PROTEINS  
; FILE REFERENCE: WALLACH-22A  
; CURRENT APPLICATION NUMBER: US/10/245,593  
; CURRENT FILING DATE: 2002-09-18  
; PRIOR APPLICATION NUMBER: US/09/927,458  
; PRIOR FILING DATE: 2001-08-13  
; PRIOR APPLICATION NUMBER: PCT/IL98/00125  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: IL 120485  
; PRIOR FILING DATE: 1997-03-19  
; PRIOR APPLICATION NUMBER: 09/381,358  
; PRIOR FILING DATE: 1999-09-20  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 522  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-245-593-2  
Query Match 100.0%; Score 2754; DB 4; Length 522;  
Best Local Similarity 100.0%; Pred. No. 2.6e-223;  
Matches 522; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MRLRVLLKRTWPLEVPETEPTLGHLSRLSLCTWGYSSNTRFTITLNYKDLPTGDE 60  
Db 1 MRLRVLLKRTWPLEVPETEPTLGHLSRLSLCTWGYSSNTRFTITLNYKDLPTGDE 60  
Qy 61 ETLASYGIVSGDLICLIQDDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNQTSMQDEQP 120  
Db 61 ETLASYGIVSGDLICLIQDDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNQTSMQDEQP 120  
Qy 121 SDSFGQAAQSGVWVNDSDMLGPSQNFEAESIQDNAHMAEGTGFYSEPMLCSESVEGQVP 180  
Db 121 SDSFGQAAQSGVWVNDSDMLGPSQNFEAESIQDNAHMAEGTGFYSEPMLCSESVEGQVP 180  
Qy 181 HSLETLQYSDACSDANDALIIVLIHLLMLESYIPQGTAKALSMPEKWLKSGVYKLYMH 240  
Db 181 HSLETLQYSDACSDANDALIIVLIHLLMLESYIPQGTAKALSMPEKWLKSGVYKLYMH 240  
Qy 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFCKEKLGENVANIYKD 300  
Db 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFCKEKLGENVANIYKD 300  
Qy 301 LQKLSRLFKDQLVYPLLAFTRAQALNLPDVFGVLVPLLELKLRIFFLLDVRSLSAVCR 360  
Db 301 LQKLSRLFKDQLVYPLLAFTRAQALNLPDVFGVLVPLLELKLRIFFLLDVRSLSAVCR 360  
Qy 361 DLFTASNDPLLRFLYLDRFDNTVRVQDQDPTLPGVGDPISSLLPGGETPSQPPPLRP 480  
Db 361 DLFTASNDPLLRFLYLDRFDNTVRVQDQDPTLPGVGDPISSLLPGGETPSQPPPLRP 480  
Qy 421 TIPFVNPPLHPRPPSSRLPGIIGGEYDQDPTLPGVGDPISSLLPGGETPSQPPPLRP 480  
Db 421 TIPFVNPPLHPRPPSSRLPGIIGGEYDQDPTLPGVGDPISSLLPGGETPSQPPPLRP 480  
Qy 481 RFDVGPPLPGNPILPGRGGNDPRFPFRPSRGRPTDGRLSFM 522  
Db 481 RFDVGPPLPGNPILPGRGGNDPRFPFRPSRGRPTDGRLSFM 522

Qy 361 DLFTASNDPLLRFLYLDRFDNTVRVQDQDPTLPGVGDPISSLLPGGETPSQPPPLRP 420  
Db 361 DLFTASNDPLLRFLYLDRFDNTVRVQDQDPTLPGVGDPISSLLPGGETPSQPPPLRP 420  
Qy 421 TIPFVNPPLHPRPPSSRLPGIIGGEYDQDPTLPGVGDPISSLLPGGETPSQPPPLRP 480  
Db 421 TIPFVNPPLHPRPPSSRLPGIIGGEYDQDPTLPGVGDPISSLLPGGETPSQPPPLRP 480  
Qy 481 RFDVGPPLPGNPILPGRGGNDPRFPFRPSRGRPTDGRLSFM 522  
Db 481 RFDVGPPLPGNPILPGRGGNDPRFPFRPSRGRPTDGRLSFM 522  
RESULT 3  
US-10-679-246-10  
; Sequence 10, Application US/10679246  
; Publication No. US20040163138A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; APPLICANT: Matsuzawa, Shu-ichi  
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved  
; FILE OF INVENTION: in Protein Degradation, Products and Methods Related Thereto  
; FILE REFERENCE: 66821-235  
; CURRENT APPLICATION NUMBER: US/10/679,246  
; CURRENT FILING DATE: 2003-10-02  
; PRIOR APPLICATION NUMBER: US 09/591,694  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 522  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-679-246-10  
Query Match 99.6%; Score 2744; DB 4; Length 522;  
Best Local Similarity 99.6%; Pred. No. 1.8e-222;  
Matches 520; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MRLRVLLKRTWPLEVPETEPTLGHLSRLSLCTWGYSSNTRFTITLNYKDLPTGDE 60  
Db 1 MRLRVLLKRTWPLEVPETEPTLGHLSRLSLCTWGYSSNTRFTITLNYKDLPTGDE 60  
Qy 61 ETLASYGIVSGDLICLIQDDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNQTSMQDEQP 120  
Db 61 ETLASYGIVSGDLICLIQDDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNQTSMQDEQP 120  
Qy 121 SDSFGQAAQSGVWVNDSDMLGPSQNFEAESIQDNAHMAEGTGFYSEPMLCSESVEGQVP 180  
Db 121 SDSFGQAAQSGVWVNDSDMLGPSQNFEAESIQDNAHMAEGTGFYSEPMLCSESVEGQVP 180  
Qy 181 HSLETLQYSDACSDANDALIIVLIHLLMLESYIPQGTAKALSMPEKWLKSGVYKLYMH 240  
Db 181 HSLETLQYSDACSDANDALIIVLIHLLMLESYIPQGTAKALSMPEKWLKSGVYKLYMH 240  
Qy 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFCKEKLGENVANIYKD 300  
Db 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFCKEKLGENVANIYKD 300  
Qy 301 LQKLSRLFKDQLVYPLLAFTRAQALNLPDVFGVLVPLLELKLRIFFLLDVRSLSAVCR 360  
Db 301 LQKLSRLFKDQLVYPLLAFTRAQALNLPDVFGVLVPLLELKLRIFFLLDVRSLSAVCR 360  
Qy 361 DLFTASNDPLLRFLYLDRFDNTVRVQDQDPTLPGVGDPISSLLPGGETPSQPPPLRP 420  
Db 361 DLFTASNDPLLRFLYLDRFDNTVRVQDQDPTLPGVGDPISSLLPGGETPSQPPPLRP 420  
Qy 421 TIPFVNPPLHPRPPSSRLPGIIGGEYDQDPTLPGVGDPISSLLPGGETPSQPPPLRP 480  
Db 421 TIPFVNPPLHPRPPSSRLPGIIGGEYDQDPTLPGVGDPISSLLPGGETPSQPPPLRP 480  
Qy 481 RFDVGPPLPGNPILPGRGGNDPRFPFRPSRGRPTDGRLSFM 522  
Db 481 RFDVGPPLPGNPILPGRGGNDPRFPFRPSRGRPTDGRLSFM 522

Db 481 RFDVPGPLPGNPILPGRGPNDRFFRPSRGRPTDGRLSFM 522

RESULT 4

US-10-042-417-14  
; Sequence 14, Application US/10042417  
; Publication No. US20020123082A1  
; GENERAL INFORMATION:  
; APPLICANT: Pagano, M.  
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF  
; TITLE OF INVENTION: PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS  
; FILE REFERENCE: 5914-090-999  
; CURRENT APPLICATION NUMBER: US/10/042,417  
; CURRENT FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: 60/260,179  
; PRIOR FILING DATE: 2001-01-5  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 482  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-042-417-14

Query Match 90.4%; Score 2489; DB 4; Length 482;  
Best Local Similarity 98.1%; Pred. No. 5.4e-201;  
Matches 472; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 42 SNTRFTITLNYKDPITGDEETLASYGIVSGDLICILLODDIPAPNIPSSSTDSEHSSLQNN 101  
Db 2 SNTRFTITLNYKDPITGDEETLASYGIVSGDLICILLODDIPAPNIPSSSTDSEHSSLQNN 61  
Qy 102 EQPSLATSSNQTSMQDEQPSDSFQQAQSGVWNNDDSMGLGFSQNFEAESIODNAHMAEGT 161  
Db 62 EQPSLATSSNQTSMQDEQPSDSFQQAQSGVWNNDDSMGLGFSQNFEAESIODNAHMAEGT 121  
Qy 162 GFYSEPMLCSESVGGVPHSLETLYQSADCSANDALIVLIHLLMLESVIGPOGTEAKA 221  
Db 122 GFYSEPMLCSESVGGVPHSLETLYQSADCSANDALIVLIHLLMLESVIGPOGTEAKA 181  
Qy 222 LSMPEKWKLSGVYKLYMHPLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLP 281  
Db 182 LSLPEKWKLSGVYKLYMHPLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLP 241  
Qy 282 ESFICKKLGENVANIYKDLQKLSRLFKQQLVYPLLAFTRAQALNLPDVGLVVLPLELKL 341  
Db 242 ESFICKKLGENVANIYKDLQKLSRLFKQQLVYPLLAFTRAQALNLPDVGLVVLPLELKL 301  
Qy 342 RIFRLLDVRSVLSLSAVCRDLFTASNDPLLRFLYLRDRDNTVVRVQDQDQRTPLPYVGDP 401  
Db 302 RIFRLLDVRSVLSLSAVCRDLFTASNDPLLRFLYLRDRDNTVVRVQDQDQRTPLPYVGDP 361  
Qy 402 QKESPKGRFVMLLPSSSTHTIPFPNPLHPRPPSSRLPGIIGGEYDQRTPLPYVGDP 461  
Db 362 QKESPKGRFVMLLPSSSTHTIPFPNPLHPRPPSSRLPGIIGGEYDQRTPLPYVGDP 421  
Qy 462 SSLLPGGETPSQPLPRLPRDPVGLPGNPILPGRGPNDRPPRPSRGRPTDGRLSF 521  
Db 422 SSLLPGGETPSQPLPRLPRDPVGLPGNPILPGRGPNDRPPRPSRGRPTDGRLSF 481  
Qy 522 M 522  
Db 482 M 482

RESULT 5

US-10-652-928-14  
; Sequence 14, Application US/10652928  
; Publication No. US20050079558A1  
; GENERAL INFORMATION:  
; APPLICANT: Chiaux, D.  
; APPLICANT: Pagano, M.  
; APPLICANT: Latres, E.

; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS  
; FILE REFERENCE: 5914-081  
; CURRENT APPLICATION NUMBER: US/10/652,928  
; CURRENT FILING DATE: 2003-08-28  
; PRIOR APPLICATION NUMBER: US/09/385,219A  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: 60/098,355  
; PRIOR FILING DATE: 1998-08-28  
; PRIOR APPLICATION NUMBER: 60/118,568  
; PRIOR FILING DATE: 1999-02-03  
; PRIOR APPLICATION NUMBER: 60/124,449  
; PRIOR FILING DATE: 1999-03-15  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 482  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-652-928-14

Query Match 90.4%; Score 2489; DB 5; Length 482;  
Best Local Similarity 98.1%; Pred. No. 5.4e-201;  
Matches 472; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 42 SNTRFTITLNYKDPITGDEETLASYGIVSGDLICILLODDIPAPNIPSSSTDSEHSSLQNN 101  
Db 2 SNTRFTITLNYKDPITGDEETLASYGIVSGDLICILLODDIPAPNIPSSSTDSEHSSLQNN 61  
Qy 102 EQPSLATSSNQTSMQDEQPSDSFQQAQSGVWNNDDSMGLGFSQNFEAESIODNAHMAEGT 161  
Db 62 EQPSLATSSNQTSMQDEQPSDSFQQAQSGVWNNDDSMGLGFSQNFEAESIODNAHMAEGT 121  
Qy 162 GFYSEPMLCSESVGGVPHSLETLYQSADCSANDALIVLIHLLMLESVIGPOGTEAKA 221  
Db 122 GFYSEPMLCSESVGGVPHSLETLYQSADCSANDALIVLIHLLMLESVIGPOGTEAKA 181  
Qy 222 LSMPEKWKLSGVYKLYMHPLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLP 281  
Db 182 LSLPEKWKLSGVYKLYMHPLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLP 241  
Qy 282 ESFICKKLGENVANIYKDLQKLSRLFKQQLVYPLLAFTRAQALNLPDVGLVVLPLELKL 341  
Db 242 ESFICKKLGENVANIYKDLQKLSRLFKQQLVYPLLAFTRAQALNLPDVGLVVLPLELKL 301  
Qy 342 RIFRLLDVRSVLSLSAVCRDLFTASNDPLLRFLYLRDRDNTVVRVQDQDQRTPLPYVGDP 401  
Db 302 RIFRLLDVRSVLSLSAVCRDLFTASNDPLLRFLYLRDRDNTVVRVQDQDQRTPLPYVGDP 361  
Qy 402 QKESPKGRFVMLLPSSSTHTIPFPNPLHPRPPSSRLPGIIGGEYDQRTPLPYVGDP 461  
Db 362 QKESPKGRFVMLLPSSSTHTIPFPNPLHPRPPSSRLPGIIGGEYDQRTPLPYVGDP 421  
Qy 462 SSLLPGGETPSQPLPRLPRDPVGLPGNPILPGRGPNDRPPRPSRGRPTDGRLSF 521  
Db 422 SSLLPGGETPSQPLPRLPRDPVGLPGNPILPGRGPNDRPPRPSRGRPTDGRLSF 481  
Qy 522 M 522  
Db 482 M 482

RESULT 6

US-11-073-485-14  
; Sequence 14, Application US/11073485  
; Publication No. US20050208601A1  
; GENERAL INFORMATION:  
; APPLICANT: Pagano, M.  
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIF  
; TITLE OF INVENTION: AND DIFFERENTIATIVE DISORDERS  
; FILE REFERENCE: 5914-090-999  
; CURRENT APPLICATION NUMBER: US/11/073,485  
; CURRENT FILING DATE: 2005-03-04  
; PRIOR APPLICATION NUMBER: 10/042,417

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; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-485-14

Query Match          90.4%; Score 2489; DB 6; Length 482;
Best Local Similarity 98.1%; Pred. No. 5.4e-201;
Matches 472; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 42 SNTRFTITLNYKDPDLTGDEETLASYGIVSGDLICLIILQDDIPAPNIPSTDSHSSLQNN 101
Db 2 SNTRFTITLNYKDPDLTGDEETLASYGIVSGDLICLIILHDDIPPPNIPSTDSHSSLQNN 61

QY 102 EQPSLATSSNOTSMQDEQPSDSFOGAAQSGVWDDSMLGPSQNFESIQDNAHMAEGT 161
Db 62 EQPSLATSSNOTSIQDEQPSDSFOGAAQSGVWDDSMLGPSQNFESIQDNAHMAEGT 121

QY 162 GFYPSEPMLCSESVGQVPHSLFTLYQSADCSANDALIIVLIHLLMLESYGVIPOGTEAKA 221
Db 122 GFYPSEPLLCSESVGQVPHSLFTLYQSADCSANDALIIVLIHLLMLESYGVIPOGTEAKA 181

QY 222 LMSPEKWKLSGVYKLYQMHPHLCGSSATLTCVPLGNLIIVNATLKINNEIRSVKRLQLLP 281
Db 182 LSLPEKWKLSGVYKLYQMHPHLCGSSATLTCVPLGNLIIVNATLKINNEIRSVKRLQLLP 241

QY 282 ESFICKEKLGENVANIYKDLQKLSRLFKDQLYVPLLAFTQALNLPVFGVLVPLELKL 341
Db 242 ESFICKEKLGENVANIYKDLQKLSRLFKDQLYVPLLAFTQALNLPVFGVLVPLELKL 301

QY 342 RIFRLDVRSLVSACVCRDLFTASNDPLLRFLYLRDFTNTVVRVQDTHKELYRKHHI 401
Db 302 RIFRLDVRSLVSACVCRDLFTASNDPLLRFLYLRDFTNTVVRVQDTHKELYRKHHI 361

QY 402 QKESPKGRFVMLPSSTHTIPFPNPLHPRFPSSRLPGIIGGEYDQRTPLPYVGDPPI 461
Db 362 QKESPKGRFVLLPSSTHTIPFPNPLHPRFPSSRLPGIIGGEYDQRTPLPYVGDPPI 421

QY 462 SSLIPGGETSPQFPLPRPDPVGPLPGNPILPGRGPNDRFPFRSGRPTDGRLSF 521
Db 422 SSLIPGGETSQLPRPDPVGPLPGNPILPGRGPNDRFPFRSGRPTDGRLSF 481

QY 522 M 522
Db 482 M 482

RESULT 7
US-11-073-470-14
; Sequence 14, Application US/11073470
; Publication No. US20050214879A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFE
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,470
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-11-073-470-14

Query Match          90.4%; Score 2489; DB 6; Length 482;
Best Local Similarity 98.1%; Pred. No. 5.4e-201;
Matches 472; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 42 SNTRFTITLNYKDPDLTGDEETLASYGIVSGDLICLIILQDDIPAPNIPSTDSHSSLQNN 101
Db 2 SNTRFTITLNYKDPDLTGDEETLASYGIVSGDLICLIILHDDIPPPNIPSTDSHSSLQNN 61

QY 102 EQPSLATSSNOTSMQDEQPSDSFOGAAQSGVWDDSMLGPSQNFESIQDNAHMAEGT 161
Db 62 EQPSLATSSNOTSIQDEQPSDSFOGAAQSGVWDDSMLGPSQNFESIQDNAHMAEGT 121

QY 162 GFYPSEPMLCSESVGQVPHSLFTLYQSADCSANDALIIVLIHLLMLESYGVIPOGTEAKA 221
Db 122 GFYPSEPLLCSESVGQVPHSLFTLYQSADCSANDALIIVLIHLLMLESYGVIPOGTEAKA 181

QY 222 LMSPEKWKLSGVYKLYQMHPHLCGSSATLTCVPLGNLIIVNATLKINNEIRSVKRLQLLP 281
Db 182 LSLPEKWKLSGVYKLYQMHPHLCGSSATLTCVPLGNLIIVNATLKINNEIRSVKRLQLLP 241

QY 282 ESFICKEKLGENVANIYKDLQKLSRLFKDQLYVPLLAFTQALNLPVFGVLVPLELKL 341
Db 242 ESFICKEKLGENVANIYKDLQKLSRLFKDQLYVPLLAFTQALNLPVFGVLVPLELKL 301

QY 342 RIFRLDVRSLVSACVCRDLFTASNDPLLRFLYLRDFTNTVVRVQDTHKELYRKHHI 401
Db 302 RIFRLDVRSLVSACVCRDLFTASNDPLLRFLYLRDFTNTVVRVQDTHKELYRKHHI 361

QY 402 QKESPKGRFVMLPSSTHTIPFPNPLHPRFPSSRLPGIIGGEYDQRTPLPYVGDPPI 461
Db 362 QKESPKGRFVLLPSSTHTIPFPNPLHPRFPSSRLPGIIGGEYDQRTPLPYVGDPPI 421

QY 462 SSLIPGGETSPQFPLPRPDPVGPLPGNPILPGRGPNDRFPFRSGRPTDGRLSF 521
Db 422 SSLIPGGETSQLPRPDPVGPLPGNPILPGRGPNDRFPFRSGRPTDGRLSF 481

QY 522 M 522
Db 482 M 482

RESULT 8
US-09-397-945-200
; Sequence 200, Application US/09397945
; Publication No. US20030065139A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: 95 Human secreted proteins
; FILE REFERENCE: P4027F1
; CURRENT APPLICATION NUMBER: US/09/397,945
; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/05804
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,566
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,576
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,573
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,574
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,579
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,314
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080,312
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/078,578
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,581
; PRIOR FILING DATE: 1998-03-19
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;; PRIOR APPLICATION NUMBER: 60/078,577  
;; PRIOR FILING DATE: 1998-03-19  
;; PRIOR APPLICATION NUMBER: 60/078,563  
;; PRIOR FILING DATE: 1998-03-19  
;; PRIOR APPLICATION NUMBER: 60/080,313  
;; PRIOR FILING DATE: 1998-04-01  
;; NUMBER OF SEQ ID NOS: 470  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 200  
;; LENGTH: 462  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: SITE  
;; LOCATION: (115)  
;; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-397-945-200

Query Match 87.3%; Score 2404; DB 3; Length 462;  
Best Local Similarity 88.1%; Pred. No. 7.6e-194;  
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;  
  
Qy 1 MRLRVRLKRTWPLEVPEPETETGLHLSHLSLLCTWGYSSNTRFTITLNYKDLPTGDE 60  
Db 1 MRLRVRLKRTWPLEVPEPETETGLHLSHLSLLCTWGYSSNTRFTITLNYKDLPTGDE 60  
  
Qy 61 ETLASYGIVSGDLICLLIQDDIPAPNIPSSSTDSEHSLQNNQPSLATSSNOTSMQDEQP 120  
Db 61 ETLASYGIVSGDLICLLIQDDIPAPNIPSSSTDSEHSLQNNQPSLATSSNOTSMQDEQP 120  
  
Qy 121 SDSFGQAAQSGVWDDSMGLPSONFEAESIQDHAHMAEGTGFYPSBPMLCSVESVEGQVP 180  
Db 121 SDSFGQAAQSGVWDDSMGLPSONFEAESIQDHAHMAEGTGFYPSBPMLCSVESVEGQVP 180  
  
Qy 181 HSLETLQSDADCSANDALIVLHLLMLESYIPOGTEAKALSMPKWKLSGVYKLYMH 240  
Db 181 HSLETLQSDADCSANDALIVLHLLMLESYIPOGTEAKALSMPKWKLSGVYKLYMH 240  
  
Qy 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKEKLGENVANIYKD 300  
Db 241 PLCEGSSATLTCVPLGNLIVVN----- 262  
  
Qy 301 LQKLSRLFKQLVYPLLAFTQALNLPDVFGLVVLPLELKLIRFRLLDVRSVLSAVCR 360  
Db 263 -----ALNLPDVFGLVVLPLELKLIRFRLLDVRSVLSAVCR 300  
  
Qy 361 DLFTASNDPILLWRFLYLDRDNTVRVQDQDTEKLYRKHIORKESPKGRFVMLLPSSSTH 420  
Db 301 DLFTASNDPILLWRFLYLDRDNTVRVQDQDTEKLYRKHIORKESPKGRFVMLLPSSSTH 360  
  
Qy 421 TIFYPNPLHPRPPSSRLPGIIGGYDQDPTLPYVGDPISSLIPOGGETPSQFPPLRP 480  
Db 361 TIFYPNPLHPRPPSSRLPGIIGGYDQDPTLPYVGDPISSLIPOGGETPSQFPPLRP 420  
  
Qy 481 RFDVPGPLPGNPILPGRGGPNDRFPFRPSRGRPTDGRLSFM 522  
Db 421 RFDVPGPLPGNPILPGRGGPNDRFPFRPSRGRPTDGRLSFM 462

RESULT 9  
US-10-264-237-2485  
;; Sequence 2485, Application US/10264237  
;; Publication No. US20040009491A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Birse et al.  
;; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
;; FILE REFERENCE: PA131P1  
;; CURRENT APPLICATION NUMBER: US/10/264,237  
;; PRIOR FILING DATE: 2002-10-04  
;; PRIOR APPLICATION NUMBER: PCT/US01/16450  
;; PRIOR FILING DATE: 2001-05-18  
;; PRIOR APPLICATION NUMBER: US 60/205,515  
;; PRIOR FILING DATE: 2000-05-19

;; NUMBER OF SEQ ID NOS: 2876  
;; SOFTWARE: PatentIn Ver. 3.1  
;; SEQ ID NO 2485  
;; LENGTH: 462  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: MISC FEATURE  
;; LOCATION: (115)  
;; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
US-10-264-237-2485

Query Match 87.3%; Score 2404; DB 4; Length 462;  
Best Local Similarity 88.1%; Pred. No. 7.6e-194;  
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;  
  
Qy 1 MRLRVRLKRTWPLEVPEPETETGLHLSHLSLLCTWGYSSNTRFTITLNYKDLPTGDE 60  
Db 1 MRLRVRLKRTWPLEVPEPETETGLHLSHLSLLCTWGYSSNTRFTITLNYKDLPTGDE 60  
  
Qy 61 ETLASYGIVSGDLICLLIQDDIPAPNIPSSSTDSEHSLQNNQPSLATSSNOTSMQDEQP 120  
Db 61 ETLASYGIVSGDLICLLIQDDIPAPNIPSSSTDSEHSLQNNQPSLATSSNOTSMQDEQP 120  
  
Qy 121 SDSFGQAAQSGVWDDSMGLPSONFEAESIQDHAHMAEGTGFYPSBPMLCSVESVEGQVP 180  
Db 121 SDSFGQAAQSGVWDDSMGLPSONFEAESIQDHAHMAEGTGFYPSBPMLCSVESVEGQVP 180  
  
Qy 181 HSLETLQSDADCSANDALIVLHLLMLESYIPOGTEAKALSMPKWKLSGVYKLYMH 240  
Db 181 HSLETLQSDADCSANDALIVLHLLMLESYIPOGTEAKALSMPKWKLSGVYKLYMH 240  
  
Qy 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKEKLGENVANIYKD 300  
Db 241 PLCEGSSATLTCVPLGNLIVVN----- 262  
  
Qy 301 LQKLSRLFKQLVYPLLAFTQALNLPDVFGLVVLPLELKLIRFRLLDVRSVLSAVCR 360  
Db 263 -----ALNLPDVFGLVVLPLELKLIRFRLLDVRSVLSAVCR 300  
  
Qy 361 DLFTASNDPILLWRFLYLDRDNTVRVQDQDTEKLYRKHIORKESPKGRFVMLLPSSSTH 420  
Db 301 DLFTASNDPILLWRFLYLDRDNTVRVQDQDTEKLYRKHIORKESPKGRFVMLLPSSSTH 360  
  
Qy 421 TIFYPNPLHPRPPSSRLPGIIGGYDQDPTLPYVGDPISSLIPOGGETPSQFPPLRP 480  
Db 361 TIFYPNPLHPRPPSSRLPGIIGGYDQDPTLPYVGDPISSLIPOGGETPSQFPPLRP 420  
  
Qy 481 RFDVPGPLPGNPILPGRGGPNDRFPFRPSRGRPTDGRLSFM 522  
Db 421 RFDVPGPLPGNPILPGRGGPNDRFPFRPSRGRPTDGRLSFM 462

RESULT 10  
US-10-653-595-200  
;; Sequence 200, Application US/10653595  
;; Publication No. US20040048304A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Ruben et. al.  
;; TITLE OF INVENTION: 95 Human secreted proteins  
;; FILE REFERENCE: P2027P1C1  
;; CURRENT APPLICATION NUMBER: US/10/653,595  
;; PRIOR FILING DATE: 2003-09-03  
;; PRIOR APPLICATION NUMBER: US 09/397945  
;; PRIOR FILING DATE: 1999-09-17  
;; PRIOR APPLICATION NUMBER: PCT/US99/05804  
;; PRIOR FILING DATE: 1999-03-18  
;; PRIOR APPLICATION NUMBER: 60/078,566  
;; PRIOR FILING DATE: 1998-03-19  
;; PRIOR APPLICATION NUMBER: 60/078,576  
;; PRIOR FILING DATE: 1998-03-19  
;; PRIOR APPLICATION NUMBER: 60/078,573  
;; PRIOR FILING DATE: 1998-03-19

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; PRIOR APPLICATION NUMBER: 60/078,574
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,579
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,314
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080,312
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/078,578
; PRIOR FILING DATE: 1998-03-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 200
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (115)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-653-595-200

Query Match      87.3%; Score 2404; DB 4; Length 462;
Best Local Similarity 88.1%; Pred. No. 7,6e-194;
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

QY 1 MRLVRLKRTWPLEVPETEPTLGHLSRLSLCTWGYSSNTFTITLNYKDLPTGDE 60
DB 1 MRLVRLKRTWPLEVPETEPTLGHLSRLSLCTWGYSSNTFTITLNYKDLPTGDE 60

QY 61 ETLASYGVSGDLICLIQDDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNQTSMQDSQP 120
DB 61 ETLASYGVSGDLICLIQDDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNQTSMQDSQP 120

QY 121 SDSFGQAAQSGVWDDSMGLPSONFEAESIQDNAHMAEGTGFYPSEPMLCSESVEGQVP 180
DB 121 SDSFGQAAQSGVWDDSMGLPSONFEAESIQDNAHMAEGTGFYPSEPMLCSESVEGQVP 180

QY 181 HSLETLYOSADCSANDALIVLIHLLMESGYIQGTAKALSMPEKWKLSGVYKLYMH 240
DB 181 HSLETLYOSADCSANDALIVLIHLLMESGYIQGTAKALSMPEKWKLSGVYKLYMH 240

QY 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPSPFCCKEKGENVANIYKD 300
DB 241 PLCEGSSATLTCVPLGNLIVVN-----ALNLPDVFGVLVPLLELKLRI 360

QY 301 LQKLSRLFKDQLVYPLLAFTQALNLPDVFGVLVPLLELKLRI 360
DB 263 -----ALNLPDVFGVLVPLLELKLRI 300

QY 361 DLFTASNDPLLRFLYLRDPRNTVRVQDTHKELYRKHRIQKESPKGRFVMLLPSSSTH 420
DB 301 DLFTASNDPLLRFLYLRDPRNTVRVQDTHKELYRKHRIQKESPKGRFVMLLPSSSTH 360

QY 421 TIPFPNPLHPRFPSSRLPGIIGGEYDQRTPLPVGDPISLLIPGGETSPQPPPLRP 480
DB 361 TIPFPNPLHPRFPSSRLPGIIGGEYDQRTPLPVGDPISLLIPGGETSPQPPPLRP 420

QY 481 RFDVPGLPGNRPILPGRGPNDRFPFRPSRGRPTDGRLSFM 522
DB 421 RFDVPGLPGNRPILPGRGPNDRFPFRPSRGRPTDGRLSFM 462

RESULT 11
US-09-397-945-435
; Sequence 435, Application US/09397945
; Publication No. US20030065139A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: 95 Human secreted proteins
; FILE REFERENCE: P2027P1
; CURRENT APPLICATION NUMBER: US/09/397,945
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; CURRENT FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/05804
; PRIOR FILING DATE: 1999-03-18
; PRIOR APPLICATION NUMBER: 60/078,566
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,576
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,573
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,574
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,579
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,314
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080,312
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/078,578
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,581
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,577
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/078,563
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 60/080,313
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 470
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 435
; LENGTH: 497
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (150)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-397-945-435

Query Match      87.3%; Score 2404; DB 3; Length 497;
Best Local Similarity 88.1%; Pred. No. 8,5e-194;
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

QY 1 MRLVRLKRTWPLEVPETEPTLGHLSRLSLCTWGYSSNTFTITLNYKDLPTGDE 60
DB 36 MRLVRLKRTWPLEVPETEPTLGHLSRLSLCTWGYSSNTFTITLNYKDLPTGDE 95

QY 61 ETLASYGVSGDLICLIQDDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNQTSMQDSQP 120
DB 96 ETLASYGVSGDLICLIQDDIPAPNIPSSSTDSEHSSLQNNQPSLATSSNQTSMQDSQP 155

QY 121 SDSFGQAAQSGVWDDSMGLPSONFEAESIQDNAHMAEGTGFYPSEPMLCSESVEGQVP 180
DB 156 SDSFGQAAQSGVWDDSMGLPSONFEAESIQDNAHMAEGTGFYPSEPMLCSESVEGQVP 215

QY 181 HSLETLYOSADCSANDALIVLIHLLMESGYIQGTAKALSMPEKWKLSGVYKLYMH 240
DB 216 HSLETLYOSADCSANDALIVLIHLLMESGYIQGTAKALSMPEKWKLSGVYKLYMH 275

QY 241 PLCEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPSPFCCKEKGENVANIYKD 300
DB 276 PLCEGSSATLTCVPLGNLIVVN-----ALNLPDVFGVLVPLLELKLRI 360

QY 301 LQKLSRLFKDQLVYPLLAFTQALNLPDVFGVLVPLLELKLRI 360
DB 298 -----ALNLPDVFGVLVPLLELKLRI 335

QY 361 DLFTASNDPLLRFLYLRDPRNTVRVQDTHKELYRKHRIQKESPKGRFVMLLPSSSTH 420
DB 336 DLFTASNDPLLRFLYLRDPRNTVRVQDTHKELYRKHRIQKESPKGRFVMLLPSSSTH 395

QY 421 TIPFPNPLHPRFPSSRLPGIIGGEYDQRTPLPVGDPISLLIPGGETSPQPPPLRP 480
DB 421 TIPFPNPLHPRFPSSRLPGIIGGEYDQRTPLPVGDPISLLIPGGETSPQPPPLRP 480
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Db 396 TIFYPNPLHPRPPSSRLPGIIGGEYDQRPTLPYVGDPISLIPGGTTPSQFPPLRP 455  
Qy 481 RFDVGPPLPGNPILPGRGGNDPFRPFRPSRGRPTDGRLSFM 522  
Db 456 RFDVGPPLPGNPILPGRGGNDPFRPFRPSRGRPTDGRLSFM 497

RESULT 12

US-10-653-595-435  
; Sequence 435, Application US/10653595  
; Publication No. US20040048304A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et. al.  
; TITLE OF INVENTION: 95 Human secreted proteins  
; FILE REFERENCE: P2027P1C1  
; CURRENT APPLICATION NUMBER: US/10/653,595  
; CURRENT FILING DATE: 2003-09-03  
; PRIOR APPLICATION NUMBER: US 09/397945  
; PRIOR FILING DATE: 1999-09-17  
; PRIOR APPLICATION NUMBER: PCT/US99/05804  
; PRIOR FILING DATE: 1999-03-18  
; PRIOR APPLICATION NUMBER: 60/078,566  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: 60/078,576  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: 60/078,573  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: 60/078,574  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: 60/078,579  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: 60/080,314  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080,312  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/078,578  
; PRIOR FILING DATE: 1998-03-19  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 470  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 435  
; LENGTH: 497  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (150)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-10-653-595-435

Query Match 87.3%; Score 2404; DB 4; Length 497;  
Best Local Similarity 88.1%; Pred. No. 8.5e-194;  
Matches 460; Conservative 0; Mismatches 2; Indels 60; Gaps 1;  
Qy 1 MRLRVLLKRTWPLEVETETPTLGLRSLRLSLCTGWYSSNTRFTITLYKDPGLTGE 60  
Db 36 MRLRVLLKRTWPLEVETETPTLGLRSLRLSLCTGWYSSNTRFTITLYKDPGLTGE 95  
Qy 61 ETLASYGIVSGDLICLLIODDIPAPNTPSSTDSEHSLQNEQPSLATSSNOTSQDEQP 120  
Db 96 ETLASYGIVSGDLICLLIODDIPAPNTPSSTDSEHSLQNEQPSLATSSNOTSQDEQP 155  
Qy 121 SDSQFQQAAGSVWDDSMGLPSONFEASIQDNAHMAEGTGFYPSBPMCLCSSEVGEQVP 180  
Db 156 SDSQFQQAAGSVWDDSMGLPSONFEASIQDNAHMAEGTGFYPSBPMCLCSSEVGEQVP 215  
Qy 181 HSLETLQYQADCSANDALIVLHLLMLESYIPQGTAKALSMPEKWLKSGVYKLYQM 240  
Db 216 HSLETLQYQADCSANDALIVLHLLMLESYIPQGTAKALSMPEKWLKSGVYKLYQM 275  
Qy 241 PLCEGSSATLTCVPLGNLIVNATLKINNEIRSVKRLQLLPESFICKEKLGENVANYIKD 300  
Db 276 PLCEGSSATLTCVPLGNLIVN----- 297

Qy 301 LQKLSRLFKDQLVYPLLAFTQALNLPDVFGLVVLPLELKLIRIFRLLDVRSVLSAVCR 360  
Db 298 -----ALNLPDVFGLVVLPLELKLIRIFRLLDVRSVLSAVCR 335  
Qy 361 DLFTASNDPPLLWRFLYLRDRFNDTVRVQDQTDWKELYKRKHIOQKESPKGRFVMLLPSTH 420  
Db 336 DLFTASNDPPLLWRFLYLRDRFNDTVRVQDQTDWKELYKRKHIOQKESPKGRFVMLLPSTH 395  
Qy 421 TIFYPNPLHPRPPSSRLPGIIGGEYDQRPTLPYVGDPISLIPGGTTPSQFPPLRP 480  
Db 396 TIFYPNPLHPRPPSSRLPGIIGGEYDQRPTLPYVGDPISLIPGGTTPSQFPPLRP 455  
Qy 481 RFDVGPPLPGNPILPGRGGNDPFRPFRPSRGRPTDGRLSFM 522  
Db 456 RFDVGPPLPGNPILPGRGGNDPFRPFRPSRGRPTDGRLSFM 497

RESULT 13

US-10-679-246-8  
; Sequence 8, Application US/10679246  
; Publication No. US20040163138A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; TITLE OF INVENTION: Nucleic Acid Encoding Proteins Involved  
; TITLE OF INVENTION: in Protein Degradation, Products and Methods Related Thereto  
; FILE REFERENCE: 66821-235  
; CURRENT APPLICATION NUMBER: US/10/679,246  
; CURRENT FILING DATE: 2003-10-02  
; PRIOR APPLICATION NUMBER: US 09/591,694  
; PRIOR FILING DATE: 2000-06-09  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: Fast-Seq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 443  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-679-246-8

Query Match 82.4%; Score 2270; DB 4; Length 443;  
Best Local Similarity 99.8%; Pred. No. 1.5e-182;  
Matches 430; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
Qy 92 DSEHSSLQNEQPSLATSSNOTSQDEQPSDFQQAAGSVWDDSMGLPSONFEASIS 151  
Db 13 DSEHSSLQNEQPSLATSSNOTSQDEQPSDFQQAAGSVWDDSMGLPSONFEASIS 72  
Qy 152 QDNAHMAEGTGFYPSBPMCLCSSEVGEQVPHSLFTLYQSADCSANDALIVLHLLMLES 211  
Db 73 QDNAHMAEGTGFYPSBPMCLCSSEVGEQVPHSLFTLYQSADCSANDALIVLHLLMLES 132  
Qy 212 YIPQGTAKALSMPEKWLKSGVYKLYQMHPCLCGSSATLTCVPLGNLIVNATLKINNEI 271  
Db 133 YIPQGTAKALSMPEKWLKSGVYKLYQMHPCLCGSSATLTCVPLGNLIVNATLKINNEI 192  
Qy 272 RSVKRLQLLPESFICKEKLGENVANYIKDQLKLSRLFKDQLVYPLLAFTQALNLPDVF 331  
Db 193 RSVKRLQLLPESFICKEKLGENVANYIKDQLKLSRLFKDQLVYPLLAFTQALNLPDVF 252  
Qy 332 LVVLPLELKLIRIFRLLDVRSVLSAVCRDLFTASNDPPLLWRFLYLRDRFNDTVRVQD 391  
Db 253 LVVLPLELKLIRIFRLLDVRSVLSAVCRDLFTASNDPPLLWRFLYLRDRFNDTVRVQD 312  
Qy 392 WKELYKRKHIOQKESPKGRFVMLLPSTHTIPIYPNPLHPRPPSSRLPGIIGGEYDQR 451  
Db 313 WKELYKRKHIOQKESPKGRFVMLLPSTHTIPIYPNPLHPRPPSSRLPGIIGGEYDQR 372  
Qy 452 PTLPYVGDPISLIPGGTTPSQFPPLRPRFPVGPPLPGNPILPGRGGNDPFRPPPSR 511  
Db 373 PTLPYVGDPISLIPGGTTPSQFPPLRPRFPVGPPLPGNPILPGRGGNDPFRPPPSR 432  
Qy 512 GRPTDGRLSFM 522

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Db 433 GRPTDGRLSFM 443
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RESULT 14
US-10-450-763-48869
; Sequence 48869, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CI3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 48869
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(549)
; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-48869

Query Match 75.8%; Score 2086.5; DB 5; Length 549;
Best Local Similarity 80.8%; Pred. No. 6.2e-167;
Matches 438; Conservative 15; Mismatches 64; Indels 25; Gaps 18;

Qy 3 LRVLKKTWPLEVET--EPTLGHRLGHLRLSLCTWGYNSNTFTITLNYKDLPTGDE 60
Db 2 LRVLKKTWPLEVETGARTPGGILRHLRQSLCTWGYNSNTFTITLNYKDLPTGDE 61
Qy 61 ETLASYGIVSGDLICLLIQDDIPAPNIPSSSTDSEHSSIQNNBPQSLATSSNQTSMDQEP 120
Db 62 ETLASYGIVSGDLICLLIQDDIPAPNIPSSSTDSEHSSIQNNBPQSLATSSNQTSMDQEP 121
Qy 121 SDSFGQAAQSGVWDDSMGLGPSQNFESIQDQNAHMAEGTGFYSEPMKLS 177
Db 122 SDSFGQAAQSGVWDDSMGLGPSQNFESIQDQNAHMAEGTGFYSEPMKLS 180
Qy 178 QVPHSLETLYQSADCSANDALIVLIHLLMLESYIPQGTAKALSMPEKWKLSGVYKIQ 237
Db 181 QVPHSLETLYQLAUCSDANDALIVLIHLLMLESYIPQGTAKALSMPEKWKLSGVYKIQ 240
Qy 238 YMHPLCEGSSATLTCVPLGNLIVVNATLKINNEIRS - VKRLQLLPESFICKEKLGENVAN 296
Db 241 YMHPLCEGSSVTLTCVPLGNLIVVNATLKINNEIRKCKKGCSSLPEFICKEKLGENVAN 300
Qy 297 IYKDLQKLSRLFKDQLVYPLLAFTQALNLPDVGVLVPLLELKLRIFRLLDVRSLVS 356
Db 301 IYKDLQKLSRLFKDQLAHLAFTQALNLPDVGVLVPLLELKLRIFRLLDVRSLVS 360
Qy 357 AVCRLDFTASNDPLLRFLYL - RDRDNTVRVQDQTDWKELY - RKRHIQRKESPKGR - F 411
Db 361 AVCRLDFTASNDPLLRVYICVNFDRNTVRVQDQTDWERTVQGRRAHTKEKESPKGRVLW 420
Qy 412 VMLPSSSTHTIPFPNPL - HPR - PFPSS - SRLPPYIGGEY - -DQRTPLPYVGDPISSLP 466
Db 421 MLLAIRQTHITIPFPYQPLWHPRGHFKLPAPPPGIYSGVWDDMQRTFPYVGRTOSSSLN 480
Qy 467 G--PGETPS - QFPPLRPDPVGP - LQGN - PILP - GRGCPNDRF - PFRPSRGR - PTDGR 518
Db 481 SWVLGETPKPSFLPLRPDPVWHPFGPPSLPRARAGPNDQISPPRPOQSGQLIGR 540
Qy 519 LS 520
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Db 541 LS 542
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RESULT 15
US-10-264-237-2484
; Sequence 2484, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2484
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-264-237-2484

Query Match 55.4%; Score 1527; DB 4; Length 317;
Best Local Similarity 94.0%; Pred. No. 4.6e-120;
Matches 300; Conservative 4; Mismatches 11; Indels 4; Gaps 2;

Qy 115 MQDEQPSDSFOGQAAQSGVWDDSMGLGPSQNFESIQDQNAHMAEGTGFYSEPMKLS 174
Db 1 MQDEQPSDSFOGQAAQSGVWDDSMGLGPSQNFESIQDQNAHMAEGTGFYSEPMKLS 60
Qy 175 VEGQVPHSLETLYQSADCSANDALIVLIHLLMLESYIPQGTAKALSMPEKWKLSGVY 234
Db 61 VEGQVPHSLETLYQSADCSANDALIVLIHLLMLESYIPQGTAKALSMPEKWKLSGVY 120
Qy 235 KLOYMHPICEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKEKLGENV 294
Db 121 KLOYMHPICEGSSATLTCVPLGNLIVVNATLKINNEIRSVKRLQLLPESFICKEKLGENV 180
Qy 295 ANIYKDLQKLSRLFKDQLVYPLLAFTQALNLPDVGVLVPLLELKLRIFRLLDVRSLVS 354
Db 181 ANIYKDLQKLSRLFKDQLVYPLLAFTQALNLPDVGVLVPLLELKLRIFRLLDVRSLVS 240
Qy 355 LSACVCRDLFTASNDPLLRFLYLDRDNTVRVQDQTDWKELYRKRHIQRKESPKGRF--V 412
Db 241 LSACVCRDLFTASNDPLLRFLYLDRDNTVRVQDQTDWKELYRKRHIQRKESPKGRVCA 300
Qy 413 MLLPSSSTHTIPFPNPLHP 431
Db 301 PAIVNSHHSI--LSOPLAP 317
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Search completed: February 14, 2006, 21:16:27

Job time : 171 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 14, 2006, 21:13:48 ; Search time 17 Seconds  
(without alignments)  
402.939 Million cell updates/sec

Title: US-09-927-458-2  
Perfect score: 2754  
Sequence: 1 MRURVLLKRTWPLEVDETE.....DRPFPRSRGRPTDGRLSFM 522

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:  
1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2489	90.4	482	6	US-10-632-150-14 Sequence 14, Appl
2	2489	90.4	482	7	US-11-073-457-14 Sequence 14, Appl
3	2489	90.4	482	7	US-11-073-460-14 Sequence 14, Appl
4	194	7.0	39	6	US-10-632-150-21 Sequence 21, Appl
5	194	7.0	39	7	US-11-073-457-21 Sequence 21, Appl
6	194	7.0	39	7	US-11-073-460-21 Sequence 21, Appl
7	139	5.0	327	6	US-10-632-150-58 Sequence 58, Appl
8	139	5.0	327	7	US-11-073-457-58 Sequence 58, Appl
9	139	5.0	327	7	US-11-073-460-58 Sequence 58, Appl
10	114.5	4.2	346	7	US-11-036-256-33 Sequence 33, Appl
11	114	4.1	2432	6	US-10-821-234-899 Sequence 899, App
12	109.5	4.0	791	6	US-10-821-234-962 Sequence 962, App
13	106.5	3.9	200	7	US-11-036-256-27 Sequence 27, Appl
14	106.5	3.9	228	7	US-11-036-256-31 Sequence 31, Appl
15	105	3.8	398	7	US-11-150-845-10 Sequence 10, Appl
16	105	3.8	398	7	US-11-150-847-10 Sequence 10, Appl
17	105	3.8	502	7	US-11-122-795-14 Sequence 14, Appl
18	105	3.8	502	7	US-11-150-845-2 Sequence 2, Appl
19	105	3.8	502	7	US-11-149-945-1 Sequence 1, Appl
20	105	3.8	502	7	US-11-150-847-2 Sequence 2, Appl
21	105	3.8	609	7	US-11-150-845-20 Sequence 20, Appl
22	105	3.8	609	7	US-11-150-847-20 Sequence 20, Appl
23	105	3.8	649	7	US-11-150-845-18 Sequence 18, Appl
24	105	3.8	649	7	US-11-150-845-22 Sequence 22, Appl
25	105	3.8	649	7	US-11-150-487-18 Sequence 18, Appl

26	105	3.8	649	7	US-11-150-487-22 Sequence 22, Appl
27	105	3.8	715	7	US-11-150-845-14 Sequence 14, Appl
28	105	3.8	715	7	US-11-150-487-14 Sequence 14, Appl
29	102.5	3.7	116	7	US-11-036-256-25 Sequence 25, Appl
30	101.5	3.7	411	7	US-11-036-256-89 Sequence 89, Appl
31	100.5	3.6	860	7	US-11-172-410-2 Sequence 2, Appl
32	100.5	3.6	915	6	US-10-821-234-1514 Sequence 1514, Ap
33	99.5	3.6	175	6	US-10-821-234-1074 Sequence 1074, Ap
34	99	3.6	552	6	US-10-821-234-1022 Sequence 1022, Ap
35	98.5	3.6	1187	6	US-10-821-234-955 Sequence 955, App
36	98	3.6	1076	6	US-10-467-557-7916 Sequence 7916, Ap
37	97.5	3.5	183	7	US-11-036-256-21 Sequence 21, Appl
38	97.5	3.5	16990	7	US-11-175-689-7 Sequence 7, Appl
39	97	3.5	1377	6	US-10-821-234-1070 Sequence 1002, Ap
40	95.5	3.5	628	6	US-10-995-561-1003 Sequence 1003, Ap
41	95.5	3.5	915	6	US-10-995-561-1003 Sequence 1003, Ap
42	95.5	3.5	917	6	US-10-995-561-1000 Sequence 1000, Ap
43	95.5	3.5	940	6	US-10-995-561-1004 Sequence 1004, Ap
44	95.5	3.5	963	6	US-10-467-962B-2 Sequence 2, Appl
45	95.5	3.5	969	6	US-10-995-561-1001 Sequence 1001, Ap

ALIGNMENTS

RESULT 1  
US-10-632-150-14  
; Sequence 14, Application US/10632150  
; Publication No. US20050251871A1  
; GENERAL INFORMATION:  
; APPLICANT: Chiaux, D.  
; APPLICANT: Pagano, M.  
; APPLICANT: Latres, E.  
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS  
; FILE REFERENCE: 5914-081  
; CURRENT APPLICATION NUMBER: US/10/632,150  
; CURRENT FILING DATE: 2003-07-30  
; PRIOR APPLICATION NUMBER: US/09/385,219  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: 60/098,355  
; PRIOR FILING DATE: 1998-08-28  
; PRIOR APPLICATION NUMBER: 60/118,568  
; PRIOR FILING DATE: 1999-02-03  
; PRIOR APPLICATION NUMBER: 60/124,449  
; PRIOR FILING DATE: 1999-03-15  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 482  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-632-150-14

Query Match 90.4%; Score 2489; DB 6; Length 482;  
Best Local Similarity 98.1%; Pred. No. 2.1e-200;  
Matches 472; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy	42	SNRFTITLNYKDPITGDEETLASYGIVSGDLICLLIQLDDIPAPNIPSSSTDSEHSSLONN	101
Db	2	SNRFTITLNYKDPITGDEETLASYGIVSGDLICLLIQLDDIPAPNIPSSSTDSEHSSLONN	61
Qy	102	EQPSLATSSNOTSMQDEQPSDSFQQAQSGVWVNDMSMLGSPQNFPAESIQDNNAHMAEGT	161
Db	62	EQPSLATSSNOTSIQDEQPSDSFQQAQSGVWVNDMSMLGSPQNFPAESIQDNNAHMAEGT	121
Qy	162	GFYPSPEMLCSSEVGVQPHSLTETLQSDACSDANDALIVLIHLLMESGYIPQGTBAKA	221
Db	122	GFYPSPEMLCSSEVGVQPHSLTETLQSDACSDANDALIVLIHLLMESGYIPQGTBAKA	181
Qy	222	LSMPEKWLKSGVVKLYQWHPHLCGSSNTLTCVPLGNLIVVNATLKINNEIRSVKRLQLLP	281
Db	182	LSLPEKWLKSGVVKLYQWHPHLCGSSNTLTCVPLGNLIVVNATLKINNEIRSVKRLQLLP	241

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Qy 282 ESFCKEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTQALNLPDVFGVLVLPLEKL 341
Db 242 ESFCKEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTQALNLPVFGVLVLPLEKL 301
Qy 342 RIFRLLDVRSVLSLSAVCRDLFTASNDPLLWRFLYLRDRFNTVRVQDQTDWKELYRKHI 401
Db 302 RIFRLLDVRSVLSLSAVCRDLFTASNDPLLWRFLYLRDRFNTVRVQDQTDWKELYRKHI 361
Qy 402 QRKESPKGRFVMLLPSSSTHTTIPFPNPLHPRPPSSRLPPGIIIGEYDQRTPLPVVGDP 461
Db 362 QRKESPKGRFVMLLPSSSTHTTIPFPNPLHPRPPSSRLPPGIIIGEYDQRTPLPVVGDP 421
Qy 462 SSLIPGCGTSPQPPPLRPDPVGPPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSF 521
Db 422 SSLIPGCGTSPQPPPLRPDPVGPPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSF 481
Qy 522 M 522
Db 482 M 482

RESULT 2
US-11-073-457-14
; Sequence 14, Application US/11073457
; Publication No. US2005026056A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIF
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,457
; PRIOR FILING DATE: 2005-03-04
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-457-14

Query Match 90.4%; Score 2489; DB 7; Length 482;
Best Local Similarity 98.1%; Pred. No. 2.1e-200;
Matches 472; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 42 SNTRFTITLNYKDPDTGDEETLASYGIVSGDLICLILODDIPAPNIPSTDSSEHSSLQNN 101
Db 2 SNTRFTITLNYKDPDTGDEETLASYGIVSGDLICLILODDIPPPNIPSTDSSEHSSLQNN 61
Qy 102 EOPSLSATSSNOTSMODEQPSDFQQAQSGVWDDSMLGPSQNFPEAESIQDNAHMAEGT 161
Db 62 EOPSLSATSSNOTSIQDEQPSDFQQAQSGVWDDSMLGPSQNFPEAESIQDNAHMAEGT 121
Qy 162 GFYSEPMCLCSVESVQVPHSLQSLFKDQLVYPLLAFTQALNLPDVFGVLVLPLEKL 221
Db 122 GFYSEPMCLCSVESVQVPHSLQSLFKDQLVYPLLAFTQALNLPDVFGVLVLPLEKL 181
Qy 222 LSMPKWKLSGVYKLYQVHPLCEGSSATLTCTVPLGNLIVVATLKINNEIRSVKRLQLLP 281
Db 182 LSLPEKWKLSGVYKLYQVHPLCEGSSATLTCTVPLGNLIVVATLKINNEIRSVKRLQLLP 241
Qy 282 ESFCKEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTQALNLPDVFGVLVLPLEKL 341
Db 242 ESFCKEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTQALNLPVFGVLVLPLEKL 301
Qy 342 RIFRLLDVRSVLSLSAVCRDLFTASNDPLLWRFLYLRDRFNTVRVQDQTDWKELYRKHI 401
Db 302 RIFRLLDVRSVLSLSAVCRDLFTASNDPLLWRFLYLRDRFNTVRVQDQTDWKELYRKHI 361
Qy 402 QRKESPKGRFVMLLPSSSTHTTIPFPNPLHPRPPSSRLPPGIIIGEYDQRTPLPVVGDP 461
Db 362 QRKESPKGRFVMLLPSSSTHTTIPFPNPLHPRPPSSRLPPGIIIGEYDQRTPLPVVGDP 421
Qy 462 SSLIPGCGTSPQPPPLRPDPVGPPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSF 521
Db 422 SSLIPGCGTSPQPPPLRPDPVGPPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSF 481
Qy 522 M 522
Db 482 M 482

RESULT 3
US-11-073-460-14
; Sequence 14, Application US/11073460
; Publication No. US2005027206A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: AND DIFFERENTIATIVE DISORDERS
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,460
; PRIOR FILING DATE: 2005-03-04
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-460-14

Query Match 90.4%; Score 2489; DB 7; Length 482;
Best Local Similarity 98.1%; Pred. No. 2.1e-200;
Matches 472; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 42 SNTRFTITLNYKDPDTGDEETLASYGIVSGDLICLILODDIPAPNIPSTDSSEHSSLQNN 101
Db 2 SNTRFTITLNYKDPDTGDEETLASYGIVSGDLICLILODDIPPPNIPSTDSSEHSSLQNN 61
Qy 102 EOPSLSATSSNOTSMODEQPSDFQQAQSGVWDDSMLGPSQNFPEAESIQDNAHMAEGT 161
Db 62 EOPSLSATSSNOTSIQDEQPSDFQQAQSGVWDDSMLGPSQNFPEAESIQDNAHMAEGT 121
Qy 162 GFYSEPMCLCSVESVQVPHSLQSLFKDQLVYPLLAFTQALNLPDVFGVLVLPLEKL 221
Db 122 GFYSEPMCLCSVESVQVPHSLQSLFKDQLVYPLLAFTQALNLPDVFGVLVLPLEKL 181
Qy 222 LSMPKWKLSGVYKLYQVHPLCEGSSATLTCTVPLGNLIVVATLKINNEIRSVKRLQLLP 281
Db 182 LSLPEKWKLSGVYKLYQVHPLCEGSSATLTCTVPLGNLIVVATLKINNEIRSVKRLQLLP 241
Qy 282 ESFCKEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTQALNLPDVFGVLVLPLEKL 341
Db 242 ESFCKEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTQALNLPVFGVLVLPLEKL 301
Qy 342 RIFRLLDVRSVLSLSAVCRDLFTASNDPLLWRFLYLRDRFNTVRVQDQTDWKELYRKHI 401
Db 302 RIFRLLDVRSVLSLSAVCRDLFTASNDPLLWRFLYLRDRFNTVRVQDQTDWKELYRKHI 361
Qy 402 QRKESPKGRFVMLLPSSSTHTTIPFPNPLHPRPPSSRLPPGIIIGEYDQRTPLPVVGDP 461
Db 362 QRKESPKGRFVMLLPSSSTHTTIPFPNPLHPRPPSSRLPPGIIIGEYDQRTPLPVVGDP 421
Qy 462 SSLIPGCGTSPQPPPLRPDPVGPPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSF 521
Db 422 SSLIPGCGTSPQPPPLRPDPVGPPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSF 481
Qy 522 M 522
Db 482 M 482
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Qy 282 ESFCKEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTQALNLPDVFGVLVLPLEKL 341
Db 242 ESFCKEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTQALNLPVFGVLVLPLEKL 301
Qy 342 RIFRLLDVRSVLSLSAVCRDLFTASNDPLLWRFLYLRDRFNTVRVQDQTDWKELYRKHI 401
Db 302 RIFRLLDVRSVLSLSAVCRDLFTASNDPLLWRFLYLRDRFNTVRVQDQTDWKELYRKHI 361
Qy 402 QRKESPKGRFVMLLPSSSTHTTIPFPNPLHPRPPSSRLPPGIIIGEYDQRTPLPVVGDP 461
Db 362 QRKESPKGRFVMLLPSSSTHTTIPFPNPLHPRPPSSRLPPGIIIGEYDQRTPLPVVGDP 421
Qy 462 SSLIPGCGTSPQPPPLRPDPVGPPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSF 521
Db 422 SSLIPGCGTSPQPPPLRPDPVGPPLPGPNPILPGRGPNDRPFRPSRGRPTDGRLSF 481
Qy 522 M 522
Db 482 M 482

RESULT 2
US-11-073-457-14
; Sequence 14, Application US/11073457
; Publication No. US2005026056A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, M.
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIF
; FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,457
; PRIOR FILING DATE: 2005-03-04
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-073-457-14

Query Match 90.4%; Score 2489; DB 7; Length 482;
Best Local Similarity 98.1%; Pred. No. 2.1e-200;
Matches 472; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 42 SNTRFTITLNYKDPDTGDEETLASYGIVSGDLICLILODDIPAPNIPSTDSSEHSSLQNN 101
Db 2 SNTRFTITLNYKDPDTGDEETLASYGIVSGDLICLILODDIPPPNIPSTDSSEHSSLQNN 61
Qy 102 EOPSLSATSSNOTSMODEQPSDFQQAQSGVWDDSMLGPSQNFPEAESIQDNAHMAEGT 161
Db 62 EOPSLSATSSNOTSIQDEQPSDFQQAQSGVWDDSMLGPSQNFPEAESIQDNAHMAEGT 121
Qy 162 GFYSEPMCLCSVESVQVPHSLQSLFKDQLVYPLLAFTQALNLPDVFGVLVLPLEKL 221
Db 122 GFYSEPMCLCSVESVQVPHSLQSLFKDQLVYPLLAFTQALNLPDVFGVLVLPLEKL 181
Qy 222 LSMPKWKLSGVYKLYQVHPLCEGSSATLTCTVPLGNLIVVATLKINNEIRSVKRLQLLP 281
Db 182 LSLPEKWKLSGVYKLYQVHPLCEGSSATLTCTVPLGNLIVVATLKINNEIRSVKRLQLLP 241
Qy 282 ESFCKEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTQALNLPDVFGVLVLPLEKL 341
Db 242 ESFCKEKLGENVANIYKDLQKLSRLFKDQLVYPLLAFTQALNLPVFGVLVLPLEKL 301
Qy 342 RIFRLLDVRSVLSLSAVCRDLFTASNDPLLWRFLYLRDRFNTVRVQDQTDWKELYRKHI 401
Db 302 RIFRLLDVRSVLSLSAVCRDLFTASNDPLLWRFLYLRDRFNTVRVQDQTDWKELYRKHI 361
Qy 402 QRKESPKGRFVMLLPSSSTHTTIPFPNPLHPRPPSSRLPPGIIIGEYDQRTPLPVVGDP 461
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Db 482 M 482

RESULT 4

US-10-632-150-21  
; Sequence 21, Application US/10632150  
; Publication No. US20050251871A1  
; GENERAL INFORMATION:  
; APPLICANT: Chiau, D.  
; APPLICANT: Pagano, M.  
; APPLICANT: Latres, E.  
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS  
; FILE REFERENCE: 5914-081  
; CURRENT APPLICATION NUMBER: US/10/632,150  
; CURRENT FILING DATE: 2003-07-30  
; PRIOR APPLICATION NUMBER: US/09/385,219  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: 60/098,355  
; PRIOR FILING DATE: 1998-08-28  
; PRIOR APPLICATION NUMBER: 60/118,568  
; PRIOR FILING DATE: 1999-02-03  
; PRIOR APPLICATION NUMBER: 60/124,449  
; PRIOR FILING DATE: 1999-03-15  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 39  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-632-150-21

Query Match 7.0%; Score 194; DB 6; Length 39;  
Best Local Similarity 100.0%; Pred. No. 3.5e-10;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 335 LPLEKLRIPLLDVRSVLSAVCRDLFTASNDPLLWR 373  
Db 1 LPLEKLRIPLLDVRSVLSAVCRDLFTASNDPLLWR 39

RESULT 5

US-11-073-457-21  
; Sequence 21, Application US/11073457  
; Publication No. US20050260556A1  
; GENERAL INFORMATION:  
; APPLICANT: Pagano, M.  
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFE  
; TITLE OF INVENTION: AND DIFFERENTIATIVE DISORDERS  
; FILE REFERENCE: 5914-090-999  
; CURRENT APPLICATION NUMBER: US/11/073,457  
; CURRENT FILING DATE: 2005-03-04  
; PRIOR APPLICATION NUMBER: 10/042,417  
; PRIOR FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: 60/260,179  
; PRIOR FILING DATE: 2001-01-05  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 39  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-073-457-21

Query Match 7.0%; Score 194; DB 7; Length 39;  
Best Local Similarity 100.0%; Pred. No. 3.5e-10;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 335 LPLEKLRIPLLDVRSVLSAVCRDLFTASNDPLLWR 373  
Db 1 LPLEKLRIPLLDVRSVLSAVCRDLFTASNDPLLWR 39

RESULT 6

US-11-073-460-21  
; Sequence 21, Application US/11073460  
; Publication No. US20050272066A1  
; GENERAL INFORMATION:  
; APPLICANT: Pagano, M.  
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLI.  
; TITLE OF INVENTION: AND DIFFERENTIATIVE DISORDERS  
; FILE REFERENCE: 5914-090-999  
; CURRENT APPLICATION NUMBER: US/11/073,460  
; CURRENT FILING DATE: 2005-03-04  
; PRIOR APPLICATION NUMBER: 10/042,417  
; PRIOR FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: 60/260,179  
; PRIOR FILING DATE: 2001-01-05  
; NUMBER OF SEQ ID NOS: 92  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 39  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-073-460-21

Query Match 7.0%; Score 194; DB 7; Length 39;  
Best Local Similarity 100.0%; Pred. No. 3.5e-10;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 335 LPLEKLRIPLLDVRSVLSAVCRDLFTASNDPLLWR 373  
Db 1 LPLEKLRIPLLDVRSVLSAVCRDLFTASNDPLLWR 39

RESULT 7

US-10-632-150-58  
; Sequence 58, Application US/10632150  
; Publication No. US20050251871A1  
; GENERAL INFORMATION:  
; APPLICANT: Chiau, D.  
; APPLICANT: Pagano, M.  
; APPLICANT: Latres, E.  
; TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS  
; FILE REFERENCE: 5914-081  
; CURRENT APPLICATION NUMBER: US/10/632,150  
; CURRENT FILING DATE: 2003-07-30  
; PRIOR APPLICATION NUMBER: US/09/385,219  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: 60/098,355  
; PRIOR FILING DATE: 1998-08-28  
; PRIOR APPLICATION NUMBER: 60/118,568  
; PRIOR FILING DATE: 1999-02-03  
; PRIOR APPLICATION NUMBER: 60/124,449  
; PRIOR FILING DATE: 1999-03-15  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 58  
; LENGTH: 327  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-632-150-58

Query Match 5.0%; Score 139; DB 6; Length 327;  
Best Local Similarity 25.1%; Pred. No. 0.00028;  
Matches 57; Conservative 32; Mismatches 64; Indels 74; Gaps 11;

Qy 291 GENVANIY----KDLQKLSRL---FKDLVYPLLAFTROALNL--PDV-----FGLVVLPL 337  
Db 19 GDGVNSYIEDNDDSKMADLLSYFQQ-----LTFQESVLKLCQPELESSQIHISVLPM 73  
Qy 338 ELKLRIPL-----LDVRSVLSAVCRDLFTASNDPLLWRFLYLRDFRONTVR-VQDTD 391  
Db 74 EVLMYIFRWVVSDDLDRSLQSLVCRGYICARDFEIRWLACKLVWGRSCIKLVPTS 133  
Qy 392 WKELYRKHITQRKESPKGRFVMLLPST-----HTIPFYPNFLHPRPF 434





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; LENGTH: 791
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-962

Query Match 4.0%; Score 109.5; DB 6; Length 791;
Best Local Similarity 20.8%; Pred. No. 0.29; Indels 109; Gaps 17;
Matches 80; Conservative 56; Mismatches 139;

Qy 17 PETE-----PTLGLHRLSHRLSLCTWGYSSNTR--FTITLN-----YKOPLT 57
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 399 PEVESLPVASSSTLLPLAPSNSTSLNSTFGSTNLTLGLFFPQLNGTANDTAGPELPPLG 458
Qy 58 G-----DEETLASGIIVSGDLICILQDDIPAPNIPSTDSHS-SLQNEQP-SLAT 108
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 459 GLLDEAMLDEISLMDLAIEG-----FNPVQASQLEEEFDSGLSDSSHSPSSLS 511
Qy 109 SSNQTNSQDEQPSDSFGQAAQSGVNDSDMLGPSQNFEAESIQDNAHMAEG-TGFVPE 167
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 512 SEGSSSSSSSSSSSSSSASSASSSFEEGAVGYSSETLDLEE-----AEGAVGYQPEY 567
Qy 168 PMLCSSEVEQVPHSLLETL-----YQSDCSDANDALIVLIHLLMLESGYIP-- 214
Db 568 SKFCRNSY-QDPAQLSCUPLYLEHVGHNHTYNAPS-----LDSADLPPP 611
Qy 215 ----QTEAKALSMPEKWLKGVYKLYQYHPLCEGSSATLTCVPLGNLIVVNATLKINNE 270
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 612 SALKGSKEKQADFQKQMSRDEHRAAMK-----IPFTNDKIINLPVEEFNE 659
Qy 271 IRSVKELQLLPESFI-----CKEKLGENVANIYKLOKLSRLFKDQLVYP 315
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 660 LLSKYQLSEQAQLSIRDIRRRGNKNMAQNCRKRLDTILNLERDVEDLQR-DKARLLRE 718
Qy 316 LLAFTRQALNL-----PDVFG 331
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 719 KVEFLSLRQMKQKVOSLYQEVFG 742

RESULT 13
US-11-036-256-27
; Sequence 27, Application US/11036256
; Publication No. US20060026719A1
; GENERAL INFORMATION:
; APPLICANT: KIELSZESWSKI, MARCIA
; APPLICANT: XU, JIANFENG
; TITLE OF INVENTION: METHODS OF PRODUCING PEPTIDES/PROTEINS IN PLANTS AND
; TITLE OF INVENTION: PEPTIDES/PROTEINS PRODUCED THEREBY
; FILE REFERENCE: 27211/04130
; CURRENT APPLICATION NUMBER: US/11/036,256
; CURRENT FILING DATE: 2005-01-14
; PRIOR APPLICATION NUMBER: 60/602,562
; PRIOR FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 60/582,027
; PRIOR FILING DATE: 2004-06-22
; PRIOR APPLICATION NUMBER: 60/536,486
; PRIOR FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 173
; SOFTWARE: Patent In Ver. 3.3
; SEQ ID NO 27
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: amino acid construct
US-11-036-256-27

Query Match 3.9%; Score 106.5; DB 7; Length 200;
Best Local Similarity 29.3%; Pred. No. 0.073;
Matches 34; Conservative 7; Mismatches 46; Indels 29; Gaps 4;

Qy 414 LLPSSHTTIPFPNP-----LHPRFPSSRLPPGIGGYDQRPTLPYVGDPISSLIPG 467
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 34 LTPLPAPTPLLLPHPGTPTLTPLPAPT-----PLLPHPGTPLTTLPL 79  
QY 458 PGETSQPPPLPRDFVGPLPGPN-PILPGRGGNDRF-----PPRPSGRP 514  
Db 80 PAPTPLLLPHPGTPTLTPLPAPTPLLLPHPGTPTLTPLPAPTPLLLPHPGTP 135

RESULT 14  
US-11-036-256-31  
; Sequence 31, Application US/11036256  
; Publication No. US20060026719A1  
; GENERAL INFORMATION:  
; APPLICANT: KIELISZEWSKI, MARCIA  
; APPLICANT: XU, JIANFENG  
; TITLE OF INVENTION: METHODS OF PRODUCING PEPTIDES/PROTEINS IN PLANTS AND  
; FILE REFERENCE: 27211/04130  
; CURRENT APPLICATION NUMBER: US/11/036,256  
; CURRENT FILING DATE: 2005-01-14  
; PRIOR APPLICATION NUMBER: 60/502,562  
; PRIOR FILING DATE: 2004-08-18  
; PRIOR APPLICATION NUMBER: 60/582,027  
; PRIOR FILING DATE: 2004-06-22  
; PRIOR APPLICATION NUMBER: 60/536,486  
; PRIOR FILING DATE: 2004-01-14  
; NUMBER OF SEQ ID NOS: 173  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 31  
; LENGTH: 228  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: amino acid construct  
US-11-036-256-31

Query Match 3.9%; Score 106.5; DB 7; Length 228;  
Best Local Similarity 33.7%; Pred. No. 0.088; Matches 35; Conservative 6; Mismatches 38; Indels 25; Gaps 4;  
QY 414 LLPSSHTIPFYFN---PLHPRPPFSSRLPPGIIGGYDQRPRTL-----PYV 457  
Db 128 LSPSTPTPPGPHSPPPPLSPSTPTPL-----GHSPPPTLSPSTPTPPPGVPVS 181  
QY 458 GDPISLLIPGGETSQPPPLPRDFVGPLPGPNPIL---PGR 498  
Db 182 GTPLPTLTPLPAPTPLLLPHPGTPTLTPLPAPTPLLLPHPGR 225

RESULT 15  
US-11-150-845-10  
; Sequence 10, Application US/11150845  
; Publication No. US20060003399A1  
; GENERAL INFORMATION:  
; APPLICANT: Cytokinetics, Inc.  
; APPLICANT: Tomasevic, Nenad  
; APPLICANT: Jia, Zhiheng  
; APPLICANT: Sakowicz, Roman  
; APPLICANT: Pierce, Daniel  
; APPLICANT: Finer, Jeffrey  
; TITLE OF INVENTION: HIGH THROUGHPUT ACTIN POLYMERIZATION ASSAY  
; FILE REFERENCE: 020552-007720US  
; CURRENT APPLICATION NUMBER: US/11/150,845  
; CURRENT FILING DATE: 2005-06-10  
; PRIOR APPLICATION NUMBER: 60/673,444  
; PRIOR FILING DATE: 2005-04-20  
; PRIOR APPLICATION NUMBER: 60/578,949  
; PRIOR FILING DATE: 2004-06-10  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 10  
; LENGTH: 398  
; TYPE: PRT

; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(398)  
; OTHER INFORMATION: 105WASP  
US-11-150-845-10  
Query Match 3.8%; Score 105; DB 7; Length 398;  
Best Local Similarity 27.3%; Pred. No. 0.26; Matches 51; Conservative 17; Mismatches 57; Indels 62; Gaps 10;  
QY 348 DVRSVLSLSAVCR-DLFTASNDPLLMRFYLRLDFRDNTRVQDQTDWKELYRKRHIQRKES 406  
Db 162 DLRSLSFSPAGISEAQLTDAETSKLIYDF-----IEDQGLEAVR-QEMRRQE- 207  
QY 407 PKGRFVMLLPSSHTTIPYPNPLHPRPPS---SRLP-PGIIGGYDQRPRTLPHYV----- 457  
Db 208 -----FLPPPPPPSRGNQLPRPPIVGGNKGSRGSLPPVPLGTA 246  
QY 458 -----GDPISLLIPGGETSQPPPLPRDFVGPLPGPNPILPGRGGNDRPFRPS 510  
Db 247 PPPPTPRGPP-----PPGRGGPP-----PPPPATGRSGPLPPPP-----PGAGGPPMPPPPPPP 296  
QY 511 RGRPTDG 517  
Db 297 PPPSSG 303

Search completed: February 14, 2006, 21:16:49  
Job time : 19 secs